

PATENT COOPERATION TREATY

PCT

INTERNATIONAL PRELIMINARY EXAMINATION REPORT

(PCT Article 36 and Rule 70)

RECEIVED 27 MAR 2001

Applicant's or agent's file reference 43922-PT	FOR FURTHER ACTION See Notification of Transmittal of International Preliminary Examination Report (Form PCT/IPEA/416)	
International application No. PCT/CA99/01202	International filing date (day/month/year) 16/12/1999	Priority date (day/month/year) 17/12/1998
International Patent Classification (IPC) or national classification and IPC C12N15/54		
Applicant NATIONAL RESEARCH COUNCIL OF CANADA et al.		


- This international preliminary examination report has been prepared by this International Preliminary Examining Authority and is transmitted to the applicant according to Article 36.
- This REPORT consists of a total of 9 sheets, including this cover sheet.

☒ This report is also accompanied by ANNEXES, i.e. sheets of the description, claims and/or drawings which have been amended and are the basis for this report and/or sheets containing rectifications made before this Authority (see Rule 70.16 and Section 607 of the Administrative Instructions under the PCT).

These annexes consist of a total of 8 sheets.

- This report contains indications relating to the following items:

- I ☒ Basis of the report
- II ☐ Priority
- III ☐ Non-establishment of opinion with regard to novelty, inventive step and industrial applicability
- IV ☐ Lack of unity of invention
- V ☒ Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement
- VI ☒ Certain documents cited
- VII ☐ Certain defects in the international application
- VIII ☒ Certain observations on the international application

Date of submission of the demand 14/07/2000	Date of completion of this report 21.03.2001
Name and mailing address of the international preliminary examining authority:  European Patent Office - P.B. 5818 Patentlaan 2 NL-2280 HV Rijswijk - Pays Bas Tel. +31 70 340 - 2040 Tx: 31 651 epo nl Fax: +31 70 340 - 3016	Authorized officer Montero Lopez, B Telephone No. +31 70 340 3739



INTERNATIONAL PRELIMINARY EXAMINATION REPORT

International application No. PCT/CA99/01202

I. Basis of the report

1. This report has been drawn on the basis of *(substitute sheets which have been furnished to the receiving Office in response to an invitation under Article 14 are referred to in this report as "originally filed" and are not annexed to the report since they do not contain amendments (Rules 70.16 and 70.17).)*:

Description, pages:

1,3-5,7-42,
44-46 as originally filed

2,2bis,6,43,47 as received on 14/12/2000 with letter of 14/12/2000

Claims, No.:

1-23 as received on 14/12/2000 with letter of 14/12/2000

Drawings, No.:

1-13 as originally filed

Sequence listing part of the description, pages:

1-20, as originally filed

2. With regard to the **language**, all the elements marked above were available or furnished to this Authority in the language in which the international application was filed, unless otherwise indicated under this item.

These elements were available or furnished to this Authority in the following language: , which is:

- ☐ the language of a translation furnished for the purposes of the international search (under Rule 23.1(b)).
- ☐ the language of publication of the international application (under Rule 48.3(b)).
- ☐ the language of a translation furnished for the purposes of international preliminary examination (under Rule 55.2 and/or 55.3).

3. With regard to any **nucleotide and/or amino acid sequence** disclosed in the international application, the international preliminary examination was carried out on the basis of the sequence listing:

- ☐ contained in the international application in written form.
- ☒ filed together with the international application in computer readable form.
- ☐ furnished subsequently to this Authority in written form.
- ☐ furnished subsequently to this Authority in computer readable form.
- ☐ The statement that the subsequently furnished written sequence listing does not go beyond the disclosure in the international application as filed has been furnished.

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- ☐ The statement that the information recorded in computer readable form is identical to the written sequence listing has been furnished.

4. The amendments have resulted in the cancellation of:

- ☐ the description, pages:
☐ the claims, Nos.:
☐ the drawings, sheets:

5. ☐ This report has been established as if (some of) the amendments had not been made, since they have been considered to go beyond the disclosure as filed (Rule 70.2(c)):
(Any replacement sheet containing such amendments must be referred to under item 1 and annexed to this report.)

6. Additional observations, if necessary:

V. Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement

1. Statement

Novelty (N)	Yes:	Claims	3-13, 17-21, 23
	No:	Claims	1, 2, 14-16, 22,
Inventive step (IS)	Yes:	Claims	5, 23
	No:	Claims	1-4, 6-22
Industrial applicability (IA)	Yes:	Claims	1-23
	No:	Claims	

2. Citations and explanations
see separate sheet

VI. Certain documents cited

1. Certain published documents (Rule 70.10)

and / or

2. Non-written disclosures (Rule 70.9)

see separate sheet

VIII. Certain observations on the international application

The following observations on the clarity of the claims, description, and drawings or on the question whether the

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claims are fully supported by the description, are made:
see separate sheet

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Re Item V

Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement

Reference is made to the following documents:

D1: R61u012 Database Entry Ac005917; Accession number AC005917; 4 November 1998; LIN X. ET AL.: "Arabidopsis thaliana chromosome II section 113 of 255 of the complete sequence"

D2: VESNA KATAVIC ET AL.: "Alteration of seed fatty acid composition by an ethyl methanesulfonate-induced mutation in Arabidopsis thaliana affecting diacylglycerol acyltransferase activity" PLANT PHYSIOLOGY, vol. 108, 1995, pages 399-409

1. Claims 1, 2 and 22 encompass a plant DNA molecule which includes, respectively, the whole or part of SEQ ID NO:1 and 3 or a sequence substantially homologous thereto.

1.1. Document D1 discloses a Arabidopsis thaliana DNA sequence identical to nucleotides 1-528 of SEQ ID NO: 1 in nucleotides 22710-23238 and to the whole SEQ ID NO:3 in nucleotides 21090-26283. This sequence is identified as encoding a diacylglycerol O-acyltransferase (see page 5 of D1). Document D1 constitutes an update of an original record submitted on 03.11.1998, subsequently updated on 19.11.1998 and 21.11.1998. These records provide corrections to the originally submitted DNA sequence. All these sequences submitted before the priority dated of the application show a high degree of homology in the fragment corresponding to nucleotides 21090-26283 with SEQ ID NOs:1 and 3. They are considered therefore to be substantially homologous thereto. Claims 1, 2 and 22 are therefore not novel and do not meet the requirements of Article 33(3) PCT.

2. Claims 3, 4, and 6-13 relate to the introduction of the DNA molecule into a vector in a sense or antisense orientation, and into plant seeds and plants. Document D1 does not disclose these particular embodiments and therefore claims 3, 4, and 6-13 are novel and comply with the requirements of Article 33(2) PCT.

2.1. The introduction of the Arabidopsis thaliana sequence disclosed in D1 into

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vectors, plant seeds and plants constitute a routine obvious application which the skilled person would put into practice using standard techniques in the art without the need of exercising any inventive skill. Consequently, claims 3, 4, and 6, 7 and 9-13 do not involve an inventive step and do not meet the requirements of Article 33(3) PCT.

2.2. Claim 8 is directed to plasmid pDGATcDNA (ATCC PTA-989). This plasmid contains the cDNA sequence disclosed in SEQ ID NO:3. Since document D1 discloses this sequence, with the exception of slight sequencing errors, the skilled person would have no difficulty in devising a plasmid equivalent to the plasmid claim in claim 8. Consequently, claim 8 lacks inventive step and does not comply with the requirements of Article 33(3) PCT.

3. Claim 5 is directed to a vector containing SEQ ID NO:23. No such sequence has been disclosed in the state of the art and therefore claim 5 is novel according to Article 33(2) PCT.

3.1. Moreover, sequence SEQ ID NO:23 is constituted by SEQ ID NO:1, containing an insertion of 81 nucleotides, for which no hint exists in the state of the art, and which the skilled person would not have been able to devise without exercising an inventive step. Claim 5, therefore, involves an inventive step according to Article 33(3) PCT.

4. Claims 14-18 relate to plant seeds and plants containing a homologous sequence to SEQ ID NO:1 and exhibiting the altered properties as described in claims 14-18.

4.1. Document D2, which is considered to represent the most relevant state of the art, discloses (cf. abstract, page 399, col. right, par. last - page 400, col. left, par. 1) an *Arabidopsis thaliana* mutant, designated AS11, which shows a reduced diacylglycerol acyltransferase activity. It is clear that the AS11 mutant disclosed in D2 contains a mutated sequence encoding diacylglycerol acyltransferase of SEQ ID NO:1; the specification in claim 11 that it consists of a recombinant sequence constitutes an attempt to define a product by its method of preparation. A particular nucleotide sequence remains the same regardless of its method of preparation. In addition, the seeds and plants disclosed in D2 show altered seed

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oil content, altered diacylglycerol content and altered fatty acyl composition (see page 402, col. left, par. 2 - col. right, par. 2 and page 403, col. left, par. 2 - page 407, col. left, par. 1). Consequently, claims 14-16 are not novel and do not meet the requirements of Article 33(2) PCT.

4.2. Claims 17 and 18 refer to plants and seeds exhibiting an enhanced biomass. Document D2 is silent about this property and therefore, claims 17 and 18 are considered to be novel and comply with the requirements of Article 33(2) PCT. However, it is considered that an enhanced biomass is an inevitable consequence of the alterations in seed oil content of the AS11 mutants. Consequently, claims 17 and 18 are considered not involve an inventive step and do not meet the requirements of Article 33(3) PCT.

5. Claims 19-21 refer to a method of producing transgenic plants by introducing into the genome of said plant a nucleotide sequence comprising SEQ ID NOs. 1 or 3 or a sequence substantially homologous thereto. Since document D1 does not disclose such an embodiment, claims 19-21 are novel and fulfill the requirements of Article 33(2) PCT.

5.1. However, the introduction of the nucleotide sequence disclosed in D1 into a plant and synthesis of a transgenic plant would be an obvious application for the skilled person which he/she would put into practice without the need of exercising any inventive step. Consequently, claims 19-21 do not involve an inventive step and do not meet the requirements of Article 33(3) PCT.

6. Claim 23 refers to a method of changing the oil content, acyl composition or diacylglycerol/triacylglycerol proportions of seed oils by transforming a plant seed with SEQ ID NO:1, 3 or 23 or a part or homologous thereof. Since document D1 does not disclose such a method, claim 23 is novel and fulfills the requirements of Article 33(2) PCT.

6.1. Sequence SEQ ID NO:3 has already been described in D1; however, its identification as encoding a diacylglycerol acyltransferase was only made after the priority date. Therefore, it would not have been obvious for the skilled person that the oil content of plant seeds can be altered by transforming them with the

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sequence disclosed in D1. Consequently, claim 23 involves an inventive step and meets the requirements of Article 33(3) PCT.

Re Item VI

Certain documents cited

Certain published documents (Rule 70.10)

Application No Patent No	Publication date (day/month/year)	Filing date (day/month/year)	Priority date (valid claim) (day/month/year)
PCT/US98/17883	29/12/1999	28/08/1998	24/06/1998
PCT/US99/15243	13/01/2000	10/06/1999	02/07/1998

Re Item VIII

Certain observations on the international application

1. Claims 1 and 2 refer to "isolated" and "purified" DNA. The degree of isolation or purification is, however, not a technical feature of a preparation and the terms "isolated" and "purified" are therefore disregarded (Article 6 PCT).

2. The relative term "substantially" used in claims 1-4, 10, 11, 19, 22 and 23 has no well-recognised meaning and leaves the reader in doubt as to the meaning of the technical features to which it refers, thereby rendering the definition of the subject-matter of said claims unclear (Article 6 PCT).

3. The term "homologous" used in claim 1-4, 10, 11, 19, 22 and 23 is vague and unclear and leaves the reader in doubt as to the meaning of the technical features to which it refers, thereby rendering the definition of the subject-matter of said claims unclear (Article 6 PCT).

6. Claims 10-13 attempt to define a product, a plant or plant seed, according to the

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process to obtain it, by introduction or transformation thereof with a recombinant nucleotide sequence. However, the method of preparation does not impart any limitation to the product . A claim directed to a product according to the process to obtain the same is therefore construed as a claim to the product as such. Claims 10-13 are considered, therefore, to encompass plants or plant seeds containing the concerned sequence irrespective of the process for their preparation (Article 6 PCT).

DGAT from cotyledons of germinating soybean seeds was reported (Kwanyuan and Wilson, 1986), detailed molecular characterization of this enzyme is lacking.

Reference is made to R61u012 Database Entry Ac005917; Accession number AC005917; 4 November 1998; LIN X. ET AL : "Arabidopsis thaliana chromosome II section 113 of 255 of the complete sequence". This relates to a nucleotide sequence deposit first submitted to the NCBI GenBank on November 3, 1998 without any identification of putative coding sequences contained therein. There was no reference in the deposited materials to a "diacylglycerol O-acyltransferase gene".

Reference is also made to VESNA KATAVIC ET AL.: "Alteration of Seed Fatty Acid Composition by an Ethyl Methanesulfonate-induced Mutation in Arabidopsis thaliana Affecting Diacylglycerol Acyltransferase Activity"; PLANT PHYSIOLOGY, vol. 108, 1995, pp. 399-409. This reference discloses an Arabidopsis mutant designated AS11 that has reduced diacylglycerol acyltransferase activity. The reference does not disclose any DNA sequences whatsoever and teaches only that alterations in DGAT activity may lead to changes in fatty acid content.

Accordingly, while the Kennedy pathway is known and shows the steps in the biosynthesis of TAGs in plants, there has not been any identification and use of a genetic element that can be used reliably in plants to modify TAG synthesis and composition in a way that may be exploited commercially.

DISCLOSURE OF THE INVENTION

An object of the invention is to identify, isolate and clone a genetic element that may be used to modify the natural formation of triacylglycerols in plants in order to increase the yield of commercial plant oils, or to modify their composition to achieve specific commercial improvements of plants and plant products.

Another object of the invention is to identify, isolate and characterize diacylglycerol acyltransferase (DGAT) gene and cDNA sequences from Arabidopsis and to utilize these sequences in the genetic manipulation of plants.

Another object of the invention is to provide a vector containing the full-length DGAT cDNA sequence from *Arabidopsis* in a sense orientation under the control of a seed-specific promoter (e.g. napin; See Josefsson et al., 1987; Radke et al., 1988; Voelker et al., 1992), for re-introducing into *Arabidopsis* or for
5 introducing into other plants.

Another object of the invention is to provide a vector containing a genomic fragment from *Arabidopsis* consisting of the full-length DGAT gene under the control of its own 5' upstream regulatory sequences, for re-introducing into *Arabidopsis* or for introducing into other plants.

10 Another object of the invention is to provide a method to construct a vector containing the full-length DGAT sequence or a significant portion of the DGAT sequence from *Arabidopsis*, in an antisense orientation under control of either a constitutive or a seed-specific promoter, for re-introducing into *Arabidopsis* or for introducing into other plants.

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expression of a full-length cDNA in yeast; (3) the characterization and isolation of the DGAT (*TAG1*) gene from *Arabidopsis* mutant AS11 containing an insertion mutation in the DGAT gene and a seed oil phenotype which consists of an altered DAG/TAG ratio, and an altered oil content and acyl composition; (4) complementation of the AS11 mutant by
5 insertion of the DGAT cDNA sequence to restore a wild-type fatty acid composition; (5) the over-expression of the DGAT cDNA in wild-type *A. thaliana* transgenic plants which produce seeds with an increased oil content, increased average seed weight and altered seed oil acyl composition.

The *A. thaliana* DGAT structure is significantly homologous (over 40% identical
10 over a region of more than 400 amino acids) to its mammalian counterparts, and is highly homologous to subsequently reported putative *B. napus* DGATs at both the nucleotide (92%) and the deduced amino acid (90%) levels (Nykiforuk et al, 1999; GenBank/EMBL Accession No AF155224; AF164434).

The DGAT of the current invention is useful in manipulating DGAT activity, and
15 triacylglycerol bioassembly in plants. For example, by transforming plants with a construct containing the DGAT gene in a sense orientation, under the control of a tissue-specific promoter (e.g. seed-specific promoter napin), the expression of DGAT and accumulation of seed oil can be enhanced or the acyl composition of the seed oil altered. Yet another example would be to express the DGAT cDNA under the control of a constitutive promoter
20 (e.g. 35S (Datla et al., 1993)) to increase the TAG content of vegetative tissues (leaves, roots, stems). This may have particular advantages for altering the starch/oil ratio in root crops.

Alternatively, DGAT expression can be silenced to some degree by anti-sense or
co-suppression (Transwitch) phenomena (De Lange et al., 1995; Mol et al., 1990;
25 Jorgensen and Napoli, 1994; Kinney, 1995; Vaucheret et al, 1998; Taylor, 1998). For example, silencing DGAT in a seed specific manner may result in a reduction in TAG accumulation. This could have applications in reducing the oil content in seed barley to enhance stability during storage. As a second example, seed-specific silencing may lead to a relatively high accumulation of DAG or an increase in the DAG/TAG ratio in the
30 developing or mature seed. As yet another example, the expression of the mutated DGAT gene which results in a 27 amino

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- Moloney, M.M., Walker, J.M. and Sharma, K.K. (1989) High efficiency transformation of *Brassica napus* using *Agrobacterium* vectors. *Plant Cell Rep.* 8: 238-242.
- Nagiec, M.M., Wells, G.B., Lester, R.L., and Dickson, R.C. (1993). A suppressor gene that enables *Saccharomyces cerevisiae* to grow without making sphingolipids encodes a protein that resembles an *Escherichia coli* fatty acyltransferase. *J. Biol. Chem.* 268, 22156-22163.
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- Nykiforuk C, Laroche A and Weselake RJ (1999) Isolation and sequence analysis of a novel cDNA encoding a putative diacylglycerol acyltransferase from a microspore-derived cell suspension culture of *Brassica napus* L. cv Jet Neuf (Accession No. AF155224)., *Plant Physiology* 120: 1207.
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- Weselake, R.J., Taylor, D.C., Pomeroy, M.K., Lawson S.L. and Underhill E.W. (1991) properties of diacylglycerol acyltransferase from microspore-derived embryos of *Brassica napus* L. *Phytochemistry* : 30: 3533-3538.
- Weselake, R.J., Pomeroy, M.K., Furukawa, T.L., Golden, J.L., Little, D.B. and Laroche, A. (1993) Developmental profile of diacylglycerol acyltransferase in maturing seeds of oilseed rape and safflower and micro-spore-derived cultures of oilseed rape. *Plant Physiol.* 102, 565-571.
- Wilson, R.F. and Kwanyuan P. (1986) Triacylglycerol synthesis and metabolism in germinating soybean cotyledons. *Biochim. Biophys. Acta* 877, 231-237.
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- Zou, J.-T., Katavic, V., Giblin, E.M., Barton, D.L., MacKenzie, S.L., Keller, W.A., Hu, X. and Taylor, D.C. (1997) Modification of seed oil content and acyl composition in the Brassicaceae by expression of a yeast sn-2 acyltransferase gene. *The Plant Cell* 9: 909-923.

CLAIMS:

1. Isolated and purified deoxyribonucleic acid (DNA), characterized in that said DNA includes a sequence according to SEQ ID NO:1 or a part of SEQ ID NO:1, or a sequence that is substantially homologous to SEQ ID NO:1.
- 5 2. Isolated and purified deoxyribonucleic acid (DNA), characterized in that said DNA includes a sequence according to SEQ ID NO:3 or a part of SEQ ID NO:3, or a sequence that is substantially homologous to SEQ ID NO:3.
3. A vector that contains a nucleic acid sequence according to SEQ ID NO:1, or a part of SEQ ID NO:1, or a sequence that is substantially homologous to
10 SEQ ID NO:1.
4. A vector that contains a nucleic acid sequence according to SEQ ID NO:3, or a part of SEQ ID NO:3, or a sequence that is substantially homologous to SEQ ID NO:3.
5. A vector that contains a deoxyribonucleic acid sequence according to
15 SEQ ID NO:23.
6. A vector according to claim 3 or claim 5, characterized in that said sequence is present in said vector in a sense orientation.
7. A vector according to claim 3, characterized in that said sequence is present in said vector in an anti-sense orientation.
- 20 8. Plasmid pDGATcDNA (ATCC PTA-989).
9. Plasmid pDGATgene (ATCC PTA-988).
10. A plant having a genome, characterized in that the genome contains an introduced recombinant nucleotide sequence of SEQ ID NO:1, or a part of SEQ ID NO:1, or a sequence that is substantially homologous to SEQ ID NO:1.
- 25 11. A plant seed having a genome, characterized in that said genome contains an introduced recombinant nucleotide sequence of SEQ ID NO:1, or a part of SEQ ID NO:1, or a sequence that is substantially homologous to SEQ ID NO:1.

12. A genetically transformed plant, characterized in that said plant has a genome that has been transformed by a vector according to claim 3 or claim 4 or claim 5.

13. A genetically transformed plant seed, characterized in that said seed
5 has been transformed by a vector according to claim 3 or claim 4 or claim 5.

14. A plant seed as claimed in Claim 11 or Claim 13, characterized by exhibiting an altered seed oil content compared to the seed oil content of seeds of genomically-unmodified plants of the same genotype grown in identical conditions at the same time.

10 15. A plant seed as claimed in Claim 11 or Claim 13, characterized by exhibiting an altered diacylglycerol content in its seed oil compared to the diacylglycerol content of seeds of genomically-unmodified plants of the same genotype grown in identical conditions at the same time.

16. A plant seed as claimed in 11 or 13, characterized by exhibiting a seed
15 oil with an altered fatty acyl composition compared to the fatty acid composition of plants of the same genotype grown in identical conditions at the same time.

17. A plant as claimed in 10 or 12, characterized by exhibiting an enhanced biomass compared to the biomass of genomically-unmodified plants of the same genotype grown in identical conditions at the same time.

20 18. A seed as claimed in 11 or 13, characterized by exhibiting an enhanced biomass compared to the biomass of genomically-unmodified plants of the same genotype grown under identical conditions at the same time.

19. A method of producing transgenic plants by introducing a recombinant nucleotide sequence into a genome of said plant, characterized in that said nucleotide
25 sequence introduced into said genome includes SEQ ID NO:1, SEQ ID NO:3 or SEQ ID NO:23; or a part of SEQ ID NO:1, SEQ ID NO:3 or SEQ ID NO:23; or a sequence that is substantially homologous to SEQ ID NO:1, SEQ ID NO:3 or SEQ ID NO:23.

20. A method according to claim 19, characterized in that said plant is a member of the Brassicaceae.

21. A method according to claim 19, characterized in that said plant is selected from the group consisting of *Arabidopsis thaliana*, borage (*Borago* spp.), Canola, castor (*Ricinus communis*), cocoa bean (*Theobroma cacao*), corn (*Zea mays*), cotton (*Gossypium* spp.), *Crambe* spp., *Cuphea* spp., flax (*Linum* spp.), *Lesquerella*
5 and *Limnanthes* spp., Linola, nasturtium (*Tropaeolum* spp.), *Oenothera* spp., olive (*Olea* spp.), palm (*Elaeis* spp.), peanut (*Arachis* spp.), rapeseed, safflower (*Carthamus* spp.), soybean (*Glycine* and *Soja* spp.), sunflower (*Helianthus* spp.), tobacco (*Nicotiana* spp.), *Vernonia* spp., wheat (*Triticum* spp.), barley (*Hordeum* spp.), rice (*Oryza* spp.), oat (*Avena* spp.) sorghum (*Sorghum* spp.), rye (*Secale* spp.) and other
10 members of the *Gramineae*.

22. An isolated plant DNA sequence or part thereof, characterized in that the sequence is substantially homologous to at least a part of SEQ ID NO:1 or SEQ ID NO:3.

15 23. A method of changing the oil content, acyl composition or diacylglycerol/triacylglycerol proportions of the seed oil of plant seeds by introducing a sense or anti-sense recombinant nucleic acid construct into a plant transformation vector, using the vector to transform the genome of a plant or plant seed, and then growing the plant or plant seed and extracting the oil from the plant seed, characterized in that said
20 recombinant nucleic acid sequence comprises SEQ ID NO:1, SEQ ID NO:3 or SEQ ID NO:23, or a part of SEQ ID NO:1, SEQ ID NO:3 or SEQ ID NO:23; or a sequence that is substantially homologous to SEQ ID NO:1, SEQ ID NO:3 or SEQ ID NO:23.

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INTERNATIONAL SEARCH REPORT

(PCT Article 18 and Rules 43 and 44)

Applicant's or agent's file reference 43922-PT	FOR FURTHER ACTION see Notification of Transmittal of International Search Report (Form PCT/ISA/220) as well as, where applicable, item 5 below.	
International application No. PCT/CA 99/ 01202	International filing date (day/month/year) 16/12/1999	(Earliest) Priority Date (day/month/year) 17/12/1998
Applicant NATIONAL RESEARCH COUNCIL OF CANADA et al.		

This International Search Report has been prepared by this International Searching Authority and is transmitted to the applicant according to Article 18. A copy is being transmitted to the International Bureau.

This International Search Report consists of a total of 5 sheets.

☒ It is also accompanied by a copy of each prior art document cited in this report.

1. Basis of the report

a. With regard to the **language**, the international search was carried out on the basis of the international application in the language in which it was filed, unless otherwise indicated under this item.

☐ the international search was carried out on the basis of a translation of the international application furnished to this Authority (Rule 23.1(b)).

b. With regard to any **nucleotide and/or amino acid sequence** disclosed in the international application, the international search was carried out on the basis of the sequence listing :

☒ contained in the international application in written form.

☒ filed together with the international application in computer readable form.

☐ furnished subsequently to this Authority in written form.

☐ furnished subsequently to this Authority in computer readable form.

☐ the statement that the subsequently furnished written sequence listing does not go beyond the disclosure in the international application as filed has been furnished.

☐ the statement that the information recorded in computer readable form is identical to the written sequence listing has been furnished

2. ☐ **Certain claims were found unsearchable** (See Box I).

3. ☐ **Unity of invention is lacking** (see Box II).

4. With regard to the **title**,

☒ the text is approved as submitted by the applicant.

☐ the text has been established by this Authority to read as follows:

5. With regard to the **abstract**,

☒ the text is approved as submitted by the applicant.

☐ the text has been established, according to Rule 38.2(b), by this Authority as it appears in Box III. The applicant may, within one month from the date of mailing of this international search report, submit comments to this Authority.

6. The figure of the **drawings** to be published with the abstract is Figure No.

☒ as suggested by the applicant.

☐ because the applicant failed to suggest a figure.

☐ because this figure better characterizes the invention.

1

☐ None of the figures.

INTERNATIONAL SEARCH REPORT

International Application No

PCT/CA 99/01202

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/54 C12N15/82 A01H5/00 A01H5/10 A01H3/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N A01H

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>R61u012 Database Entry Ac005917 Accession number AC005917; 4 November 1998 LIN X. ET AL.: "Arabidopsis thaliana chromosome II section 113 of 255 of the complete sequence" XP002133608 nucleotides 21090-23400 -& LIN X. ET AL. : "Sequence and analysis of chromosome II of Arabidopsis thaliana" NATURE, vol. 402, 1999, pages 761-768, XP000877287 LONDON GB</p> <p style="text-align: center;">---</p> <p style="text-align: center;">-/--</p>	<p>1-4, 6-8, 10-13, 19-23</p>

☒ Further documents are listed in the continuation of box C.

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INTERNATIONAL SEARCH REPORT

International Application No

CA 99/01202

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>CASES S ET AL: "Identification of a gene encoding an acyl CoA: diacylglycerol acyltransferase, a key enzyme in triacylglycerol synthesis" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA,US,NATIONAL ACADEMY OF SCIENCE. WASHINGTON, vol. 95, no. 22, 27 October 1998 (1998-10-27), pages 13018-13023, XP002122745 ISSN: 0027-8424 cited in the application the whole document</p>	1,2,22
X	<p>VESNA KATAVIC ET AL.: "Alteration of seed fatty acid composition by an ethyl methanesulfonate-induced mutation in Arabidopsis thaliana affecting diacylglycerol acyltransferase activity" PLANT PHYSIOLOGY, vol. 108, 1995, pages 399-409, XP002915657 cited in the application page 399, right-hand column, last paragraph -page 400, left-hand column, paragraph 1 page 402, left-hand column, paragraph 2 -right-hand column, paragraph 1 page 403, right-hand column, last paragraph -left-hand column, paragraph 1 page 405, right-hand column, last paragraph -page 408, left-hand column, paragraph 1</p>	10-18
E	<p>WO 99 67403 A (THE REGENTS OF THE UNIVERSITY OF CALIFORNIA) 29 December 1999 (1999-12-29) page 3, line 27 -page 6, line 5 page 10, line 2 - line 25 page 14, line 16 - line 21 page 15, line 24 -page 16, line 28 page 33, line 4 - line 32 page 39, line 28 -page 40, line 11</p>	1-4,6, 10,12, 19-23
E	<p>WO 00 01713 A (CALGENE LLC) 13 January 2000 (2000-01-13) page 4, line 10 - line 17 page 4, line 20 -page 5, line 2 page 11, line 27 -page 24, line 21; examples 11-14,16</p>	1-4,6, 10,12, 19,22,23

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INTERNATIONAL SEARCH REPORT

International Application No.

T/CA 99/01202

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	<p>Empln Database Entry Ath238008 Accession number AJ238008; 18 June 1999 ZOU J. ET AL.: "The Arabidopsis thaliana TAG1 gene encodes for a diacylglycerol acyltransferase" XP002133609 cited in the application the whole document</p> <p>---</p>	1,2,22
P,X	<p>ZOU, JITAO ET AL: "The Arabidopsis thaliana TAG1 mutant has a mutation in a diacylglycerol acyltransferase gene" PLANT J. (1999), 19(6), 645-653 , XP002133607 the whole document</p> <p>---</p>	1,2,22
P,X	<p>EMBL Database Entry AF155224 Accession number AF155224; 30 June 1999 NYKIFORUK C.L. ET AL.: "Brassica napus putative diacylglycerol cyltransferase (DGAT2) mRNA" XP002133639 cited in the application the whole document & NYKIFORUK C.L. ET AL.: "Isolation and sequence analysis of a novel cDNA encoding a putative diacylglycerol acyltransferase from a microspore-derived cell suspension culture of Brassica napus L. cv Jet Neuf (Accession No. AF155224) (PGR99-123)." PLANT PHYSIOLOGY, vol. 120, no. 4, 1999, pages 1207-1207, LONDON GB</p> <p>---</p>	1,2,22
P,X	<p>EMBL Database Entry AF164434 Accession number AF164434; 26 July 1999 NYKIFORUK C.L. ET AL.: "Brassica napus putative diacylglycerol acyltransferase (DGAT1) mRNA" XP002133640 cited in the application the whole document & NYKIFORUK C.L. ET AL.: "Isolation and characterization of a cDNA encoding a second putative diacylglycerol acyltransferase from a microspore-derived cell suspension culture of Brassica napus L. cv Jet Neuf (Accession No. AF164434) (PGR99-158)" PLANT PHYSIOLOGY, vol. 121, no. 3, 1999, pages 1053-1053,</p> <p>---</p> <p>-/--</p>	1,2,22

INTERNATIONAL SEARCH REPORT

International Application No

CT/CA 99/01202

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	HOBBS D H ET AL: "Cloning of a cDNA encoding diacylglycerol acyltransferase from Arabidopsis thaliana and its functional expression" FEBS LETTERS,NL,ELSEVIER SCIENCE PUBLISHERS, AMSTERDAM, vol. 452, no. 3, 11 June 1999 (1999-06-11), pages 145-149, XP002122747 ISSN: 0014-5793 the whole document ---	1,2,22
P,X	WO 99 63096 A (CALGENE LLC) 9 December 1999 (1999-12-09) page 3, line 24 -page 4, line 17 page 6, line 13 -page 8, line 16 page 12, line 30 -page 20, line 10; examples 1-4,7,8 sequence listing SEQ ID NO:1 -----	1-4,6, 10-13, 19,22,23

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

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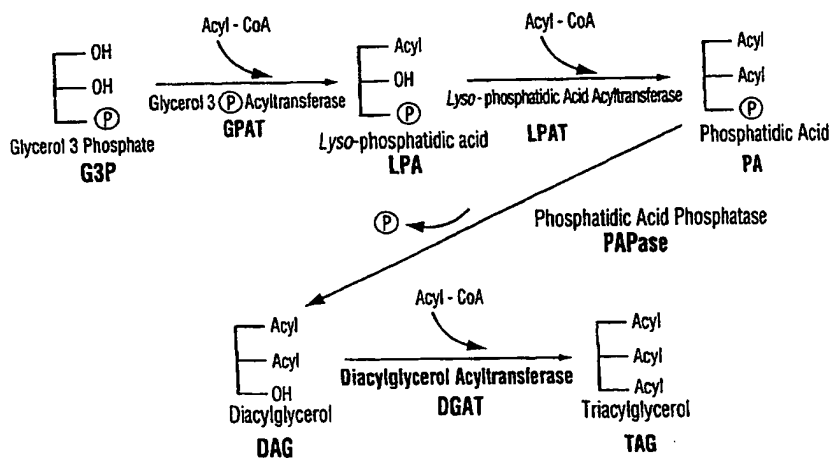
Patent document cited in search report		Publication date	Patent family member(s)	Publication date
WO 9967403	A	29-12-1999	WO 9967268 A	29-12-1999
WO 0001713	A	13-01-2000	NONE	
WO 9963096	A	09-12-1999	NONE	



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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(74) Agents: GALE, Edwin, J. et al.; Kirby, Eades, Gale, Baker, Box 3432, Station D, Ottawa, Ontario K1P 6N9 (CA).		Published With international search report. Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments. With an indication in relation to deposited biological material furnished under Rule 13bis separately from the description.	

(54) Title: DIACYLGLYCEROL ACYLTRANSFERASE GENE FROM PLANTS



(57) Abstract

The present invention relates to the isolation, purification, characterization and use of the plant diacylglycerol acyltransferase (DGAT) gene and genetic products. For example, the invention provides DGAT cDNA [SEQ ID NO:1] (pDGATcDNA; ATCC No PTA-989) and a plant diacylglycerol acyltransferase gene [SEQ ID NO:3] (pDGATgene; ATCC No PTA-988) from the Brassicaceae (specifically *Arabidopsis thaliana*). The invention includes isolated and purified DGAT DNA, preferably of the stated sequences and homologues, and relates to methods of regulating seed oil content, the ratio of diacylglycerol/triacylglycerol proportions in the seed oil, fatty acid synthesis, seed oil acyl composition, seed size/weight and carbon flux into other seed components, using the gene, and to tissues and plants transformed with the gene. The invention also relates to transgenic plants, plant tissues and plant seeds having a genome containing an introduced DNA sequence of the invention, and a method of producing such plants and plant seeds. The invention also relates to [SEQ ID NO:1] containing an 81 bp insertion [SEQ ID NO:23], and uses thereof to modify oil content, acyl composition of triacylglycerols, seed size or carbon flux into other seed components.

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DIACYLGLYCEROL ACYLTRANSFERASE GENE FROM PLANTS

TECHNICAL FIELD

This invention relates to plant genes useful for the genetic manipulation of plant characteristics. More specifically, the invention relates to the identification, isolation and introduction of diacylglycerol acyltransferase (DGAT) genes useful, for example, for altering the seed oil content, the ratio of diacylglycerol / triacylglycerol proportions in the seed oil, fatty acid synthesis, seed oil acyl composition, seed size/weight and carbon flux into other seed components, in commercial or crop plants.

10 BACKGROUND ART

Plant seed oils are major sources of essential polyunsaturated fatty acids for human diets and renewable feedstocks for chemical industries. The enzymes of the fatty acid synthase complex in the plastids of developing seeds are responsible for the biosynthesis of fatty acids that are channeled into the cytosolic acyl-CoA pool to sustain triacylglycerol accumulation. Triacylglycerol (TAG) biosynthesis is located in the endoplasmic reticulum with glycerol-3-phosphate and fatty acyl-CoAs as the primary substrates. There are three acyltransferases involved in the plant storage lipid bioassembly, namely the glycerol-3-phosphate acyltransferase (GPAT, EC 2.3.1.15), the lyso-phosphatidic acid acyltransferase (LPAT, EC 2.3.1.51) and the diacylglycerol acyltransferase (DGAT, EC 2.3.1.20). These three acyltransferases catalyze the stepwise acylation of the glycerol backbone with the final step being the acylation of *sn*-1, 2-diacylglycerol (DAG) by DGAT into the formation of TAGs, a biochemical process generally known as the Kennedy pathway (Stymne and Stobart, 1987).

25 Among the three ER-based fatty acyl-CoA acyltransferases, only LPAT gene(s) have been cloned from plants (Knutzon *et al.*, 1995, Lassner *et al.*, 1995). Like several other enzymes involved in storage lipid biosynthesis, acyltransferases are intrinsic ER proteins and are extremely difficult to purify. The research on plant DGAT has been largely limited to studies of activity profiles by using the particulate fractions generated by differential centrifugation of seed or microspore-derived embryo homogenates (Weselake *et al.*, 1993). Although partial purification of

DGAT from cotyledons of germinating soybean seeds was reported (Kwanyuan and Wilson, 1986), detailed molecular characterization of this enzyme is lacking.

Accordingly, while the Kennedy pathway is known and shows the steps in the biosynthesis of TAGs in plants, there has not been any identification and use of
5 a genetic element that can be used reliably in plants to modify TAG synthesis and composition in a way that may be exploited commercially.

DISCLOSURE OF THE INVENTION

An object of the invention is to identify, isolate and clone a genetic element that may be used to modify the natural formation of triacylglycerols in plants in order
10 to increase the yield of commercial plant oils, or to modify their composition to achieve specific commercial improvements of plants and plant products.

Another object of the invention is to identify, isolate and characterize diacylglycerol acyltransferase (DGAT) gene and cDNA sequences from *Arabidopsis* and to utilize these sequences in the genetic manipulation of plants.

15 Another object of the invention is to provide a vector containing the full-length DGAT cDNA sequence from *Arabidopsis* in a sense orientation under the control of a seed-specific promoter (e.g. napin; See Josefsson et al., 1987; Radke et al., 1988; Voelker et al., 1992), for re-introducing into *Arabidopsis* or for introducing into other plants.

20 Another object of the invention is to provide a vector containing a genomic fragment from *Arabidopsis* consisting of the full-length DGAT gene under the control of its own 5' upstream regulatory sequences, for re-introducing into *Arabidopsis* or for introducing into other plants.

Another object of the invention is to provide a method to construct a vector
25 containing the full-length DGAT sequence or a significant portion of the DGAT sequence from *Arabidopsis*, in an antisense orientation under control of either a constitutive or a seed-specific promoter, for re-introducing into *Arabidopsis* or for introducing into other plants.

Another object of the invention is to provide a method of modifying *Arabidopsis* and other plants to change their seed oil content.

Another object of the invention is to provide a method of modifying *Arabidopsis* and other plants to change the acyl composition of their seed oil.

- 5 Another object of the invention is to provide a method of modifying *Arabidopsis* and other plants to change their average seed weight or size.

According to one aspect of the present invention, there is provided a vector containing isolated and purified deoxyribonucleic acid (cDNA) of SEQ ID NO:1 (pDGATcDNA; ATCC No PTA-989), for introduction of the cDNA in a sense
10 orientation into a plant cell.

As another aspect of the present invention, there is provided a vector containing isolated and purified genomic deoxyribonucleic acid (genomic DNA) of SEQ ID NO:3 (pDGATgene; ATCC No PTA-988), for introduction of the gene in a sense orientation into a plant cell.

- 15 According to yet another object of the invention, there is provided a method for preparing a vector containing SEQ ID NO:1 or a part thereof, for introduction of the gene or partial gene in an antisense orientation, into a plant cell.

According to yet another object of the invention, there is provided seed of *Arabidopsis thaliana* ecotype Columbia mutant AS11 (ATCC No. PTA-1013) and
20 characterization of its lipid phenotype (Katavic et al., 1995; Zou et al. 1999). The AS11 mutant seed line has an insertion mutation at the *TAG1* locus on chromosome II, and produces plants exhibiting reduced DGAT activity (Figure 4) and an reduced TAG/DAG ratio during seed development (Table 1), resulting in an altered seed fatty acyl composition (Figure 2), reduced oil content (Table 1), and
25 increased seed oil diacylglycerol content during development (Figure 3) and at maturity (lower TAG/DAG ratio of Table 1). The cDNA sequence of the AS11 DGAT is shown in SEQ ID NO:23, the genomic DNA sequence is shown in SEQ ID NO:24 and the translated protein sequence of the AS11 DGAT is shown in SEQ ID NO:25.

The invention also relates to transgenic plants and plant seeds having a genome containing an introduced DNA sequence of SEQ ID NO:1 or SEQ ID NO:3, and a method of producing such plants and plant seeds.

The invention also relates to SEQ ID NO:1 or SEQ ID NO:3, or a part of
5 SEQ ID NO:1 or SEQ ID NO:3, or SEQ ID NO:1 containing an 81 bp insertion [SEQ ID NO: 23] or SEQ ID NO:3 containing an 147 bp insertion [SEQ ID NO:24] such that the deduced amino acid sequence of the encoded protein contains the repeated sequence SHAGLFNLCVVLIAVNSRLIENLMK [SEQ ID NO:25] where the spacing and identity of the underlined amino acids are identical or are replaced
10 by conserved substitutions, characterized in that said sequence has been introduced in sense or antisense orientation, and a method of producing such plants and plant seeds.

As will be appreciated by persons skilled in the art, the invention also relates to substantially homologous DNA sequences from plants encoding proteins with
15 deduced amino acid sequences of 25% or greater identity, and 40% or greater similarity, isolated and/or characterized and/or designed by known methods using the sequence information of SEQ ID NO:1 or SEQ ID NO:3 or or SEQ ID NO:1 containing an 81 bp insertion [SEQ ID NO:23] such that the deduced amino acid sequence of the encoded protein contains the repeated sequence
20 SHAGLFNLCVVLIAVNSRLIENLMK (SEQ ID NO:25) where the spacing and identity of the underlined amino acids are identical or are replaced by conserved substitutions, and to parts of reduced length that are still able to function as inhibitors of gene expression by use in an anti-sense, co-suppression (Transwitch; Jorgensen and Napoli 1994) or other gene silencing technologies. It will be
25 appreciated by persons skilled in the art that small changes in the identities of nucleotides in a specific gene sequence may result in reduced or enhanced effectiveness of the genes and that, in some applications (e.g. anti-sense or co-suppression), partial sequences often work as effectively as full length versions. The ways in which the gene sequence can be varied or shortened are well known to
30 persons skilled in the art, as are ways of testing the effectiveness of the altered genes. All such variations of the genes are therefore claimed as part of the present invention.

Other preferred degrees of identity to the indicated sequences are at least 30%, 40%, 50%, 60%, 70%, 80%, 90% and 95%; and other preferred degrees of similarity are at least 50%, 60%, 70%, 80%, 90% and 95%. The inventors have used a computer program known as MegAlign®, DNASTAR® of DNASTAR Inc.,
5 1228 South Park Street, Madison, WI 53715, USA, for assessing homology. This program is based on the Clustal V algorithm (Higgins and Sharp (1998): A package for performing multiple sequence alignment on a microcomputer; GENE 73:237-244). For each gap introduced in the alignment, the program deducts a penalty from the score. A higher gap penalty suppresses gapping; a lower value promotes
10 it. The program also assesses penalties based on the length of the gap. The more residues the gap spans, the greater the penalty. The program deducts these penalties from the overall score of the alignment.

Stated more generally, the present invention relates to the isolation, purification and characterization of a diacylglycerol acyltransferase (DGAT) gene
15 from the *Brassicaceae* (specifically *Arabidopsis thaliana*) and demonstrates its utility in regulating fatty acid synthesis, seed oil content, diacylglycerol/triacylglycerol ratios and seed size/weight. Until now, no concrete data is available on the gene structure of plant DGATs, or their utility in altering oil content or composition through genetic manipulation.

20 When considering altered oil contents or compositions, results from averages of statistically-significant numbers of plants or seeds according to the invention are best compared with results from averages of statistically-significant numbers of untransformed (control) plants or seeds of the same genotype grown under identical conditions at the same time. This allows for the variability of
25 individual plants of the same genotype, particularly when such plants are grown under different conditions. The actual number of plants or seeds used to form the required average may vary, but should be enough to provide a generally constant average whenever such number is selected. Generally, the number should be at least 10, and is more preferably at least 20, 30, 50 or 100.

30 The DGAT gene was cloned, characterized and authenticated from *Arabidopsis* by: (1) selection and characterization of plant ESTs sharing some homology to mammalian acyl-CoA: cholesterol acyltransferases; (2) the functional

- expression of a full-length cDNA in yeast; (3) the characterization and isolation of the DGAT (*TAG1*) gene from Arabidopsis mutant AS11 containing an insertion mutation in the DGAT gene and a seed oil phenotype which consists of an altered DAG/TAG ratio, and an altered oil content and acyl composition; (4)
- 5 complementation of the AS11 mutant by insertion of the DGAT cDNA sequence to restore a wild-type fatty acid composition; (5) the over-expression of the DGAT cDNA in wild-type *A. thaliana* transgenic plants which produce seeds with an increased oil content, increased average seed weight and altered seed oil acyl composition.
- 10 The *A. thaliana* DGAT structure is significantly homologous (over 40% identical over a region of more than 400 amino acids) to its mammalian counterparts, and is highly homologous to subsequently reported putative *B. napus* DGATs at both the nucleotide (92%) and the deduced amino acid (90%) levels (Nikyiforuk et al, 1999; GenBank/EMBL Accession No AF155224; AF164434).
- 15 The DGAT of the current invention is useful in manipulating DGAT activity, and triacylglycerol bioassembly in plants. For example, by transforming plants with a construct containing the DGAT gene in a sense orientation, under the control of a tissue-specific promoter (e.g. seed-specific promoter napin), the expression of DGAT and accumulation of seed oil can be enhanced or the acyl composition of the
- 20 seed oil altered. Yet another example would be to express the DGAT cDNA under the control of a constitutive promoter (e.g. 35S (Datla et al., 1993)) to increase the TAG content of vegetative tissues (leaves, roots, stems). This may have particular advantages for altering the starch/oil ratio in root crops.
- Alternatively, DGAT expression can be silenced to some degree by anti-
- 25 sense or co-suppression (Transwitch) phenomena (De Lange et al., 1995; Mol et al., 1990; Jorgensen and Napoli, 1994; Kinney, 1995; Vaucheret et al, 1998; Taylor, 1998). For example, silencing DGAT in a seed specific manner may result in a reduction in TAG accumulation. This could have applications in reducing the oil content in seed barley to enhance stability during storage. As a second example,
- 30 seed-specific silencing may lead to a relatively high accumulation of DAG or an increase in the DAG/TAG ratio in the developing or mature seed. As yet another example, the expression of the mutated DGAT gene which results in a 27 amino

- acid repeat insertion in the mutant DGAT protein (See Figure 5 a) can be used to alter the DAG/TAG ratio in developing and mature seed. Such manipulations can lead to edible seed oils produced naturally in the plant, containing enhanced relative levels of DAG /reduced levels of TAG (See Figure 3; Table 1) to act as all-natural
- 5 emulsifiers in the food and confections industries, or to enhance the nutritional/health profile of vegetable oils as functional foods (e.g. as cooking oils, stir fry oils, in salad dressings, margarines etc.) by inhibiting neutral fat deposition in humans. Processed oils produced from canola and soybean which contain increased proportions of diacylglycerol have been cited by the Kao Corporation of
- 10 Japan (e.g. Econa Cooking Oil; Kao Corporation KI, 1-14-10 Nihonbashi-Kayabacho, Chuoku, Tokyo 103 Japan; e-mail: 210064@kastanet.kao.co.jp) as a product making it difficult for blood neutral fat to increase after a meal, and for fat to cling to the body, thereby assisting individuals who are overweight or who suffer from high neutral fat levels. As a third example, silencing or reducing the activity of
- 15 DGAT in a seed specific manner (as observed in mutant AS11; e.g. by over-expressing SEQ ID NO:23 or silencing expression of SEQ ID NO:1 or SEQ ID NO:3), and combining this trait with the capacity to produce polyhydroxyalkanoates (PHAs; e.g. polyhydroxybutyrate) in seeds (Poirier et al., 1992; 1995) will allow an increased flow of unesterified fatty acids towards β -oxidation (Poirier et al., 1999).
- 20 By recycling or diverting the unesterified fatty acids into β oxidation, the resulting acetyl-CoA moieties will lead to a significant increase in polyhydroxyalkanoates (PHAs) or a change in PHA composition (Poirier et al., 1999). Transgenic plants producing PHAs in seeds have potential for utility as biodegradable thermoplastics. However, up to now, the levels of PHAs produced have been relatively small
- 25 (Poirier et al, 1992; 1995). The utility of transgenically reducing the DGAT activity to significantly enhance PHA production (e.g. 10-fold increase) in PHA-producing seeds is now possible, due to the current DGAT invention.

- Some of the manipulations and deliverables which are possible using the DGAT gene or a part thereof, include, but are not limited to, the following: seeds with
- 30 increased or decreased oil content; seeds containing oils with an enhanced diacylglycerol content, seed oils with an altered acyl composition; plants producing larger or heavier seeds; plants exhibiting an enhanced or altered capacity to accumulate storage compounds in other storage organs (e.g. tubers, roots).

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a diagram illustrating the Kennedy pathway for the bioassembly of triacylglycerols in plants, and shows the critical role played by DGAT as the final step of the Kennedy pathway.

5 Figure 2 is a graph showing the comparison of the fatty acid composition of seed oil from wild-type (WT) and DGAT mutant AS11 lines of *Arabidopsis thaliana*. Proportions of fatty acids are reported as Mol % of the total fatty acid composition of the seed oil from each line. Error bars are \pm SE (n= 10 plants of each line sampled, with 50 seeds per sample per analysis).

10 Figure 3 is a graph showing a comparison of the DAG content in developing seed of wild-type (WT) and DGAT mutant AS11 lines of *Arabidopsis thaliana*. More specifically, it is a comparison of the fatty acid content of DAG pool in wild-type green developing seeds compared to that of the AS11 mutant.

Figure 4 is a graph showing a comparison of the DGAT activity
15 (pmol/min/mg protein) in developing seeds at the milky, early green, mid-green and brown-green stages of embryo development in wild-type (WT) and DGAT mutant AS11 lines of *Arabidopsis thaliana*. Developing seeds at each stage were selected and DGAT enzyme analyses conducted as described previously by Katavic et al., 1995).

20 Figure 5(a) shows the amino acid sequence alignment of the *Arabidopsis* DGAT (AtTAG1) [SEQ ID NO:2] with mammalian (mouse and putative human) DGATs. MDGAT, mouse DGAT [SEQ ID NO:4]; GenBank/EMBL Accession No. AF078752 (Cases et al., 1998); HARGP1, human ARGP1 protein [SEQ ID NO:5]; GenBank/EMBL Accession No. AF059202; Oelkers et al., 1998]. Dots indicate
25 gaps. Identical amino acid residues are highlighted in black. Conserved residues are shaded. The 27-amino acid repeat found in *Arabidopsis thaliana* mutant AS11 and generated by the insertion mutation (81 bp) found in SEQ ID NO:23 (SHAGLFNLCVVVLIIVNSRLIENLMK) is overlined thus: _____. The putative diacylglycerol binding site is overlined thus: _____. The SnRK1 targeting site is
30 overlined thus: _____ with an asterisk (*) over the serine (S) residue as the targeted phosphorylation site.

Figure 5(b) shows the Kyte-Doolittle hydropathy plot of the DGAT protein.

Figure 6(a) shows the results of a Northern analysis of *TAG1* gene expression in *Arabidopsis thaliana*. Total RNA was extracted from roots (RT), leaves (LF), flowers (FL), young seedlings (YS), developing siliques (SL), and
5 germinating seeds (GS).

Figure 6(b) shows the results of Southern blot analysis of the *TAG1* gene in *Arabidopsis thaliana*. Genomic DNA was digested with restriction enzymes BglII (Lane 1), EcoRI (Lane 2), and HindIII (Lane 3). The *TAG1* DNA probe was ³²P labeled by random priming.

10 Figure 7(a) is a diagrammatic representation of the *TAG1* gene structure. The boxes indicate the 16 exons (solid boxes for coding regions, open box for untranslated regions), and the lines represent the 15 introns. A, B and C denote the positions of the primers used for PCR amplifications of the segments from wild type (WT) and AS11. The specific primers A, B and C are described in Experimental
15 Procedures: *Primer Strategy* (found later in this specification).

Fig 7(b) shows gel separation of the PCR products amplified from wild type (WT) and AS11. Lane 1, PCR product with primers A and B using WT genomic DNA as template. Lane 2, PCR product with primers A and B using AS11 genomic DNA as template. Lane 3, PCR product with primers C and B using WT genomic
20 DNA as template. Lane 4, PCR product with primers C and B using AS11 genomic DNA as template. Lane 5, RT-PCR with primers A and B using RNA prepared from WT seedling RNA. Lane 6, RT-PCR with primers A and B using RNA prepared from AS11 seedling RNA.

Figure 8 is a graph showing microsomal DGAT activity in Yeast Strain YMN5
25 Transformed with empty plasmid (pYES Con) and with the *A. thaliana* DGAT cDNA (pYES:DGAT). This illustrates the expression of the *TAG1* cDNA in yeast. Host cultures of strain YMN5 were transformed with pYES2 plasmid only (pYES2; without *TAG1* insert) or with pYES2 containing the *TAG1* cDNA insert (pYES2:TAG1). Following induction in the presence of galactose, transformants were lysed and
30 assayed for DGAT activity as described in the Experimental Procedures. The results of two separate DGAT activity experiments are shown.

Figure 9 is a map of plasmid pSE129A which may be used as a vector. The vector contains the following salient features for plant transformation in the current invention: the seed-specific napin promoter and NOS terminator between which is a multiple cloning site.

5 Figure 10 is a graph showing the complementation of the AS11 DGAT mutation with the wild-type cDNA. Transformation of *Arabidopsis thaliana* mutant line AS11 with the DGAT cDNA [SEQ ID NO:1] under the control of a napin promoter, leads to a restoration of the wild-type (WT) fatty acid composition in the seed oil of the transformant lines 3-4, 9-1, 14-2 and 9-4. Fatty acid composition (wt
10 %) was determined on the seed oil extracted from 100-seed samples from *A. thaliana* non-transformed controls (WT), mutant line AS11, and T₂ seeds of napin:DGAT transgenic lines.

Figure 11 is a graph showing the seed oil content of non-transformed WT control, and pRD400 control (empty plasmid) and napin:DGAT T₂ transgenic
15 *Arabidopsis thaliana* seed lines. More particularly, the graph shows the transformation of wild type (WT) *Arabidopsis thaliana* with the DGAT cDNA [SEQ ID NO:1] under the control of a napin promoter, leads to a higher seed oil content in the DGAT transgenic lines. Oil content is expressed as µg total fatty acids (FAs) per
20 100 seeds from *A. thaliana* non-transformed controls (WT Con), and T₂ seeds of pRD400 control (empty plasmid) transgenic, and napin:DGAT transgenic lines 1', 2', 9, 10 and 11. Standard error bars for the control lines are indicated; n=10.

Figure 12 is a graph showing the average 100-seed weight of non-transformed WT control, and pRD400 control (empty plasmid) and napin:DGAT T₂ transgenic *Arabidopsis thaliana* seed lines. More specifically, the graph shows the
25 over-expression of the DGAT cDNA under the control of a napin promoter, in wild-type (WT) *Arabidopsis thaliana* leads to a higher average seed weight. The average weight of 100-seed samples from *A. thaliana* non-transformed controls (WT Con), and T₂ seeds of pRD400 control (empty plasmid) transgenic, and napin:DGAT transgenic lines 1', 2', 9, 10 and 11 are reported as mg dry weight (DW).

30 Figure 13 is a graph showing the positive correlation between oil content (expressed as µg Total fatty acids (FAs) per 100 seeds) and average seed weight (expressed as average mg DW per 100-seed samples) from *A. thaliana* non-

transformed controls (WT Con ♦), and T2 seeds of pRD400 control (empty plasmid) transgenic (○) and napin:DGAT transgenic lines 1', 2', 9, 10 and 11 (■) are reported as mg dry weight (DW).

BEST MODES FOR CARRYING OUT THE INVENTION

5 Fig. 1 is a diagram illustrating the Kennedy pathway for the biosynthesis of TAGs in plants. Of the various illustrated enzymes, DGAT is the only enzyme in the Kennedy pathway that is exclusively committed to TAG biosynthesis, and its key role is apparent from the scheme of Figure 1. *sn*-1,2-DAG, generated as a result of either the catalytic action of PA phosphatase (EC 3.1.3.4) or CPTase (EC 2.7.8.2),
10 can be used in the biosynthesis of TAG.

For this reason, the inventors of the present invention decided to investigate DGAT to see if the corresponding gene in plants could be sequenced and cloned and used to modify the seed oil content and fatty acid composition of plants in a way that could be commercially useful.

15 The acyl-CoA dependent acylation of *sn*-1,2-DAG is catalyzed by DGAT (Stymne and Stobart, 1987). In developing and germinating seeds of oilseed plants, TAG accumulation and DGAT activity have been shown to associate with the endoplasmic reticulum (ER; high speed microsomal fraction) (Stobart et al., 1986; Cao and Huang, 1986; Stymne and Stobart, 1987; Frentzen, 1993; Settlage et al.,
20 1995; Lacey and Hills, 1996). The biochemical properties of microsomal DGAT have been examined in a number of plant systems (Frentzen, 1993) including developing seeds (Bernerth and Frentzen, 1990; Vogel and Browse, 1996; Cao and Huang, 1987) and embryo cultures (Taylor et al., 1991; Weselake et al., 1991; Taylor et al., 1992; Little et al., 1994) of *B. napus* L. In general, studies with developing seeds
25 indicate that DGAT activity increased rapidly during the active phase of oil accumulation and then decreases markedly as seed lipid content reaches a plateau (Tzen et al., 1993; Weselake et al., 1993).

A number of studies with both mammalian (Mayorek et al., 1989; Tijburg et al., 1989) and plant (Ichihara et al., 1988; Perry and Harwood, 1993 a and 1993 b;
30 Settlage et al. 1995) systems have suggested that DGAT may catalyze a rate-limiting reaction in TAG bioassembly. However, this hypothesis has not been

rigorously tested, and has not been reduced to practice by transgenic expression of any DGAT gene in plant or animal systems, until now. Developing seeds of *B. napus* L., cv Shiralee, have been shown to produce significant levels of DAG during the active phase of oil accumulation suggesting that DGAT catalyzed
5 reaction may regulate the flow of carbon into TAG (Perry and Harwood, 1993 a and 1993 b). In addition, an ethyl methanesulfonate-induced (EMS-induced) mutant of *A. thaliana*, designated AS11, has been shown to have a reduced DGAT activity that correlated with both an increased DAG pool and decreased accumulation of TAG (Katavic et al. 1995). Given its possible rate-limiting role in TAG bioassembly,
10 the inventors of the present invention have identified DGAT as a potential target in the genetic modification of plant lipid biosynthesis.

Previously, the partial characterization of an EMS-induced *Arabidopsis thaliana* mutant, AS11, with altered fatty acid composition was reported (Katavic et al., 1995). In comparison to wild type plant seeds, AS11 seeds have reduced levels
15 of the very long chain fatty acid eicosenoic acid (20:1) and reduced oleic acid (18:1) and accumulate α -linolenic acid (18:3) as the major fatty acid in triacylglycerols (Figure 2). The AS11 mutant has a consistently lower ratio of TAG/DAG in developing seeds, and it accumulates an elevated amount of seed DAG (Figure 3), the substrate of the diacylglycerol acyltransferase. Through a series of biochemical
20 analyses, it was shown that AS11 had reduced diacylglycerol acyltransferase activities throughout seed development (Figure 4). AS11 also had a reduced (by 25-30%) oil content phenotype, providing some evidence that DGAT may be controlling flux into TAG biosynthesis, as shown in Table 1 below. The AS11 did not have a wrinkled-seed phenotype as described in other low-seed-oil mutants (Focks
25 and Benning, 1998).

Table 1

Comparison of AS11 [Katavic et al., (1995) and wild-type *A. thaliana* seeds with respect to lipid profiles at mid-development, and the relative TAG, DAG and sterol ester contents in AS11 and WT seeds at maturity.

Seed Type	TAG/DAG ratio at mid-development ^a	TAG/DAG ratio at maturity ^a	Relative TAG content at maturity ^b ^c (nmol/mg DW)	Sterol Esters at maturity (% of Total Lipid Extract) ^d
WT	17	90	1.00 ^b ^c (255)	0.8
AS11	5	20	0.6 ^b ^c (174)	1.15

^a Embryos staged and lipids measured as described in Katavic et al., (1995);

^b Relative TAG content of 200-seed samples of AS11 and WT were measured by MASS-1H-NMR according to the method of Rutar (1989). The integration response for resonances attributable to liquid-like oil were summed and the value for AS11 seed is reported relative to the response for the WT control seed sample (the latter set at a value of 1.00); ^c TAG content (nmol/mg DW) measured by transmethylation of a TLC-purified TAG fraction, followed by GC analysis of fatty acid methyl esters; ^d A total lipid extract was prepared as described by Taylor et al., (1991; 1992), and sterol esters isolated and characterized as described in the Experimental Procedures.

Genetic analysis indicated that the fatty acid phenotype is caused by a semidominant mutation in a nuclear gene, designated *TAG1*. The mutation was mapped to chromosome II, and was estimated to lie in the region approximately 17.5 ± 3 cM from the *sti* locus and 8 ± 2 cM from the *cp2* locus.

- 5 Because a DGAT gene has not heretofore been cloned from any plant, until now, it has not been possible to address the possibility of genetic modifications to alter carbon flux, increase fatty acid synthesis, oil content, oil acyl composition, or seed size, by modulating plant DGAT activity.

- 10 However, there are many examples of successful modifications to plant metabolism that have been achieved by genetic engineering to transfer new genes or to alter the expression of existing genes, in plants. It is now routinely possible to introduce genes into many plant species of agronomic significance to improve crop performance (e.g. seed oil or tuber starch content/composition; meal improvement;

herbicide, disease or insect resistance; heavy metal tolerance etc.) (MacKenzie and Jain, 1997; Budziszewski et al., 1996; Somerville, 1993; Kishore and Somerville, 1993).

For example, increases in the proportions of some strategic fatty acids and
5 in the quantities of seed oil have been achieved by the introduction of various fatty acid biosynthesis and acyltransferase genes in oilseed crops. These include the following demonstrations: Expression of an anti-sense construct to the stearoyl-ACP $\Delta 9$ desaturase in Brassicaceae led to an increase in the stearic acid content (Knutzon et al., 1992). Expression of a medium chain fatty acyl-ACP thioesterase
10 from California Bay, in Brassicaceae was demonstrated to increase the lauric acid (12:0) content (Voelker et al., 1992; 1996). Expression of a Jojoba β keto-acyl-CoA synthase in low erucic acid Brassicaceae led to an increase the level of erucic acid (22:1); the effect following expression in high erucic acid cultivars was negligible (Lassner et al., 1996). Increased proportions of oleic acid in Brassica napus and in
15 soybean have been achieved by silencing the microsomal FAD2 ($\Delta 12$) desaturase (Hitz et al., 1995; Kinney, 1995 ; 1997). Transformation of Arabidopsis thaliana and rapeseed (B. napus) with a yeast sn-2 acyltransferase resulted in seed oils with increased proportions of 22:1 and other very long-chain fatty acids and significant increases in seed oil content (Zou et al., 1997).

20 Starch deposition has also been altered by genetic engineering. By expression of a mutant E. coli glgC16 gene encoding an ADP glucose pyrophosphorylase in potato tubers, an increase in starch accumulation was achieved (Stark et al., 1992).

The inventors therefore considered the DGAT gene to hold great promise for
25 the desired modification of TAGs in plants.

The best modes for carrying out the invention will be apparent from the following description of the results of tests and experiments that have been carried out by the inventors.

The inventors chose to use the well-accepted model plant system
30 *Arabidopsis thaliana* for the cloning of DGAT, as a host system for genetic engineering to alter DGAT expression, and to study the effects of altering DGAT

expression on seed triacylglycerol bioassembly. This is because, over the past several years, *Arabidopsis thaliana*, a typical flowering plant, has gained increasing popularity as a model system for the study of plant biology. As a result of the ease with which this plant lends itself to work in both classical and molecular genetics,

5 *Arabidopsis* has come to be widely used as a model organism in plant molecular genetics, development, physiology and biochemistry (Meyerowitz and Chang, 1985; Meyerowitz, 1987; Goodman et al., 1995). This model dicotyledonous plant is also closely related to *Brassica* crop species and it is increasingly apparent that information concerning the genetic control of basic biological processes in

10 *Arabidopsis* will be transferable to other species (Lagercrantz et al., 1996).

Indeed, there are numerous examples wherein studies of the molecular biology and biochemistry of a particular metabolic pathway or developmental process and the possibility of genetically engineering a plant to bring about changes to said metabolic pathway or process, has first been tested in the model plant

15 *Arabidopsis*, and then shown to yield similar phenotypes in other plants, particularly crop plants.

For example, the extra- plastidial membrane associated oleate (18:1) Δ^{12} (ω -6) desaturase gene, *FAD2*, was originally studied and eventually cloned from *Arabidopsis thaliana*, by identifying the lesion found in an *A. thaliana* mutant

20 defective in desaturating oleate to produce linoleate (18:2) on the phosphatidylcholine backbone. This resulted in a high oleic acid phenotype in the *A. thaliana* seed oil (Okuley et al., 1994). Genetic engineering of both soybean (*Glycine max.*) and canola *B. napus* to silence the indigenous *FAD2* gene(s) in a seed-specific manner by anti-sense or co-suppression approaches, resulted in

25 similar high oleic acid seed oil phenotypes (Kinney, 1995; 1997).

Transgenic expression of a yeast *sn*-2 acyltransferase (*SLC1-1*) gene to achieve enhanced seed oil and very long-chain fatty acid content was first performed in *Arabidopsis* and later shown to yield similar phenotypes in transgenic rapeseed (*B. napus*) experiments (Zou et al., 1997). *Arabidopsis thaliana* has

30 repeatedly shown itself to be a useful model system for metabolic engineering of metabolic pathways (e.g. lipid biosynthesis, photosynthesis) or processes (organogenesis, reproductive development etc.) common to all higher plants.

In the area of secondary metabolism/signal transduction, an anthocyanin pathway-specific transcriptional activator from the monocot maize designated as *R* (the *myc* transcription factor involved in activation of biosynthetic genes for anthocyanin production in the aleurone cells of maize kernels), was expressed in
5 the dicot *Arabidopsis*, causing augmented anthocyanin pigmentation in the inflorescences. Subsequent expression in another dicot, tobacco (*Nicotiana tabacum*), resulted in similar floral pigmentation changes (Lloyd et al., 1992). These experiments demonstrate that whole pathways common to all flowering plants can be co-ordinately controlled through the introduction of transcriptional regulators, and
10 that the mechanisms are common to diverse plant species.

In the context of the current invention, all plant seeds accumulate some triacylglycerol (oil) and this ubiquitous process is affected, at least in part, by the activity of a microsomal DGAT, as explained previously. Thus, many of the effects observed following genetic engineering to modulate DGAT expression in
15 *Arabidopsis* can be expected and predicted to result in similar phenotypes when carried out in all other plants. For example, after the present invention was made, information has become available that supports the findings of the present inventors by showing that *B. napus* has a highly homologous DGAT gene (Nikiforuk et al., 1999), and thus *B. napus* is a clear target for similar genetic modifications as those
20 shown for *A. thaliana*.

There are a number of ways by which genes and gene constructs can be introduced into plants, and a combination of plant transformation and tissue culture techniques have been successfully integrated into effective strategies for creating transgenic crop plants. These methods, which can be used in the present
25 invention, have been extensively reviewed elsewhere (Potrykus, 1991; Vasil, 1994; Walden and Wingender, 1995; Songstad et al., 1995), and are well known to persons skilled in the art. For example, one skilled in the art will certainly be aware that, in addition to *Agrobacterium*-mediated transformation of *Arabidopsis* by vacuum infiltration (Bechtold et al., 1993) or wound inoculation (Katavic et al.,
30 1994), it is equally possible to transform other plant and crop species, using *Agrobacterium* Ti-plasmid-mediated transformation (e.g. hypocotyl (DeBlock et al., 1989) or cotyledonary petiole (Moloney et al., 1989) wound infection), particle bombardment/biolistic methods (Sanford et al., 1987; Nehra et al., 1994; Becker et

al., 1994) or polyethylene glycol-assisted protoplast transformation (Rhodes et al., 1988; Shimamoto et al., 1989) methods.

As will also be apparent to persons skilled in the art, and as extensively reviewed elsewhere (Meyer, 1995; Datla et al., 1997), it is possible to utilize plant promoters to direct any intended up- or down-regulation of transgene expression using constitutive promoters (e.g. those based on CaMV35S), or by using promoters which can target gene expression to particular cells, tissues (e.g. napin promoter for expression of transgenes in developing seed cotyledons), organs (e.g. roots), to a particular developmental stage, or in response to a particular external stimulus (e.g. heat shock).

Particularly preferred plants for modification according to the present invention include *Arabidopsis thaliana*, borage (*Borago* spp.), Canola, castor (*Ricinus communis*), cocoa bean (*Theobroma cacao*), corn (*Zea mays*), cotton (*Gossypium* spp.), *Crambe* spp., *Cuphea* spp., flax (*Linum* spp.), *Lesquerella* and *Limnanthes* spp., Linola, nasturtium (*Tropaeolum* spp.), *Oenothera* spp., olive (*Olea* spp.), palm (*Elaeis* spp.), peanut (*Arachis* spp.), rapeseed, safflower (*Carthamus* spp.), soybean (*Glycine* and *Soja* spp.), sunflower (*Helianthus* spp.), tobacco (*Nicotiana* spp.), *Vernonia* spp., wheat (*Triticum* spp.), barley (*Hordeum* spp.), rice (*Oryza* spp.), oat (*Avena* spp.) sorghum (*Sorghum* spp.), rye (*Secale* spp.) or other members of the *Gramineae*.

The present invention is particularly useful when used to modify the yield or composition of oilseed produced from oilseed crops. Oilseed crops are plant species that are capable of generating edible or industrially useful oils in commercially significant yields, and include many of the plant species listed above. Such oilseed crops are well known to persons skilled in the art.

RESULTS

Isolation of the TAG1 (DGAT) cDNA from Arabidopsis thaliana

Since one of the most likely defects in AS11 mutant is at the DGAT itself (Table 1; Fig 4), the inventors attempted cloning strategies based on sequence information of enzymes that share common substrates with DGAT. One of the

candidate enzymes that would serve this purpose is the acyl-CoA: cholesterol acyltransferase (ACAT, EC 2.3.1.26) (Chang *et al.*, 1997). Like DGAT, ACAT is an ER protein functioning as an O-acyltransferase by using acyl-CoA as the fatty acyl donor for the esterification of free cholesterol to generate sterol esters. Through a
5 BLAST database search, the inventors identified an *Arabidopsis thaliana* expressed sequence tag (EST) [accession no. AA042298; SEQ ID NO:6] with a deduced amino acid sequence showing 41 % identity to that of the yeast acyl-CoA: cholesterol acyltransferase (Yang *et al.*, 1996, Yu *et al.*, 1996), within the short sequence (104 amino acids) that was available for the EST.

10 The corresponding cDNA (E6B2T7) clone was obtained from the Arabidopsis Biological Resource Center, Columbus, Ohio. Upon complete sequencing, the 878 bp E6B2T7 clone was found to be a partial cDNA. However, the ORF prediction from this partial cDNA confirmed the initial EST search results in that the encoded product is structurally similar to ACAT, especially in the regions at
15 the C-terminus. The inventors were confident that the cDNA contained the 3' untranslated region through an ORF search, although the polyA tail was missing.

The inventors further used the partial cDNA sequence to search against *Arabidopsis thaliana* genomic sequence information. An *Arabidopsis* 'IGF' BAC clone 'F27F23' [accession no. AC003058] was identified to include a region that
20 matched the cDNA, and therefore it was concluded that this was the region encompassing the corresponding gene. Moreover, this BAC clone 'F27F23', is contained in the YAC clone, CIC06E08, which, according to the published map position (http://weeds.mgh.harvard.edu/goodman/c2_b.html), represents a region between centimorgan 35.9 and centimorgan 38.7 on chromosome II; this position is
25 similar to the estimated location for *TAG1*, and the lesion identified by the mutation in AS11 (Katavic *et al.*, 1995). In view of our previous results on the characterization of the AS11 mutant, the map position of this gene strongly suggested that it may encode a DGAT.

To clone a full-length cDNA, a series of oligonucleotide primers were
30 designed, based on the genomic sequences located at different positions 5' upstream of the region covering the partial cDNA. We used these primers in combination with a primer located at the 3' UTR of the partial cDNA (E6B2T7) to

perform PCR reactions with cDNA phagemid prepared from an *Arabidopsis thaliana* (ecotype Columbia) silique-specific cDNA library (Giraudat et al., 1992) as a template. The longest cDNA amplified was 1904 bp, which we subsequently designated as TAG1, and deposited into the Genbank under accession AJ238008

5 [SEQ ID NO:1]. We believe this cDNA represents a full-length clone because its size is in agreement with that of the transcript detected in the northern blot (see Figure 6 a). The longest open reading frame is flanked by a 134-nucleotide 5' untranslated region and a 203-nucleotide 3' untranslated region. There is an in-frame stop codon (TGA at position nt-43) which is followed by an in-frame ATG at

10 position nt-139. It is thus inferred that the ATG at position nt-139 is the initiation codon.

The primary structure of TAG1 predicts a DGAT-related enzyme

The predicted open reading frame of the TAG1 cDNA encodes for a polypeptide of 520 amino acids with a calculated molecular weight of 58993

15 Daltons. With the BLAST search program (Altschul et al. 1990), it was found that the recently reported mouse diacylglycerol acyltransferase [accession no. AF078752] (Cases et al., 1998) is a protein which showed the highest sequence similarity to the deduced amino acid sequence of TAG1 (Figure 5a). TAG1 was also similar to a human acyl CoA: cholesterol acyltransferase-related enzyme

20 [accession no. AF059202]. The human acyl CoA: cholesterol acyltransferase-related enzyme, also known as ARGP1, is most likely to be a DGAT with no significant ACAT activity, although the true nature of the enzyme awaits further confirmation (Oelkers et al., 1998). The similarity between TAG1 and the mammalian DGAT extends over a region of more than 400 amino acids with a

25 sequence identity of about 41%. A putative diacylglycerol/phorbol ester-binding motif, HKW-X-X-RH-X-Y-X-P, a signature sequence observed to be unique to DGAT while absent in the ACATs (Oelkers et al., 1998), is located at amino acids 414-424 ([SEQ ID NO: 7]; Figure 5 a). This diacylglycerol binding motif is also found in the subsequently published *B. napus* DGAT sequences (Nikyiforuk et al, 1999;

30 GenBank /EMBL Accession Nos. AF155224, SEQ ID NO:8; AF164434, SEQ ID NO:9). Among other cloned acyltransferases (e.g. GPATs, LPATs, dihydroxyacetone phosphate acyltransferases) it has been reported that there is an invariant proline in a highly hydrophobic block IV that may participate in acyl-CoA

binding (Lewin et al., 1999). In the TAG1 sequence, the hydrophobic block from residues 221-229 containing an invariant proline at residue 224, might constitute such a motif.

TAG1 showed some sequence similarity to other acyl CoA: cholesterol
5 acyltransferases from a number of species (Chang et al., 1997). However, the similarity is largely confined to the C-terminus and is lower (around 30%) than is the similarity of TAG1 to the mammalian DGAT.

The TAG1 protein has multiple hydrophobic domains (Figure 5b) and an analysis by the PC Gene program predicted that the protein has 5 possible
10 transmembrane segments (amino acids 178-195, 233-253, 363-388, 433-476, 486-507). In the mammalian DGAT, a putative tyrosine phosphorylation motif was observed (Cases et al., 1998), but no apparent tyrosine phosphorylation site could be found in TAG1. However, a visual examination revealed a consensus sequence (X-L²⁰⁰-X-K²⁰²-X-X-S²⁰⁵-X-X-X-V²⁰⁹; SEQ ID NO:10) identified as a targeting motif
15 typical of members of the SnRK1 protein kinase family, with serine residue 205 being the residue for phosphorylation. The SnRK1 (SNF1-related protein kinase-1) proteins are a class of Ser/Thr protein kinases that have been increasingly implicated in the global regulation of carbon metabolism in plants (Halford and Hardie, 1998). This consensus SnRK1 targeting motif is also found in the
20 subsequently published *B. napus* DGAT sequences (Nikyforuk et al, 1999; GenBank /EMBL Accession Nos. AF155224; AF164434). Interestingly, similar SnRK1 targeting motifs could also be identified in the lyso-phosphatidic acid acyltransferases (LPATs) from coconut (Knutzon et al., 1995) and meadowfoam (Lassner et al., 1995), respectively.

25 *The TAG1 gene is ubiquitously expressed in Arabidopsis*

Northern blot analyses were performed to investigate the expression profile of the TAG1 gene. Total RNA was extracted from different tissues, including roots, leaves, flowers, developing siliques, young seedlings and germinating seeds. The highest steady-state level accumulation of TAG1 transcript was in RNA isolated
30 from germinating seeds and young seedlings (Figure 6a). TAG1 transcripts were also detected in root, leaf and flower tissues, albeit at lower levels. Surprisingly, the TAG1 gene is expressed in developing siliques at a level that is comparable to that

of other vegetative tissues, but lower than that of germinating seeds and young seedlings. This expression profile in general is not inconsistent with the notion that DGAT is present in all plant tissues capable of TAG biosynthesis (Kwanyuan and Wilson, 1986). It has been shown in a number of plant species, including soybean and safflower, that germinating seeds actively synthesize TAGs (Ichihara and Noda, 1981; Kwanyuan and Wilson, 1986; Wilson and Kwanyuan, 1986). The relatively high level of expression in roots is also consistent with the fact that root plastids are capable of synthesizing large amounts of triacylglycerol (Sparace et al., 1992).

Southern blot hybridization (Southern, 1975) was performed with genomic DNA digested with several restriction enzymes including BglII, EcoRI and HindIII. The *TAG1* gene has no internal BglII and HindIII site, while one internal EcoRI site exists. Our Southern analysis suggested that *TAG1* most likely represents a single copy gene in the *Arabidopsis* genome (Figure 6b).

An insertion mutation is found in the TAG1 gene in mutant AS11

Alignment of the genomic sequence (accession no. AC003058; SEQ ID NO:3) with that of the *TAG1* cDNA [SEQ ID NO:1] revealed that the *TAG1* gene contains 16 exons and 15 introns, spanning a region of about 3.4 kb (Figure 7a). DNA containing the *TAG1* allele from AS11 was PCR-amplified and completely sequenced. The AS11 *TAG1* allele has a 147-bp insertion located at the central region of intron 2. The insertion is a duplication of a segment that is composed of 12 bp from the 3' end of intron 1, the entire sequence of exon 2 (81 bp) and 54 bp from the 5' end of intron 2 (Figure 7a).

In order to rule out the possibility of PCR artifacts, two sets of primers were used to perform further PCR amplifications. Primers A and B (see Experimental Procedures, *Primer Strategy*) located in exons 1 and 3, respectively, amplified a DNA fragment that is about 150 bp longer from AS11 (Figure 7b, lane 2) than that from the wild type (Figure 7b, lane 1). The second pair of primers, C and B (Experimental Procedures), with one to be found in both exon 2 and the insertion segment, and the other located in exon 3, generated two amplified fragments from AS11 (Figure 7b, lane 4), while only one from the wild type (Figure 7b, lane 3). Hence these results confirmed that the insertion mutation the inventors identified

through sequencing, reflected the true nature of the mutation in the *TAG1* gene in the AS11 genome.

The AS11 TAG1 transcript has an 81-bp insertion in its open reading frame

Northern blot analyses indicated that there was no difference in the
5 expression profiles of the *TAG1* gene, between the AS11 mutant and wild type *A. thaliana*. In order to investigate the effect of the mutation at the transcript level, reverse-transcription PCR (RT-PCR) was performed to amplify the *TAG1* transcript from RNA extracted from germinating seedlings of mutant AS11. Sequencing
analysis revealed that there is an 81-bp insertion composed entirely of exon 2 in the
10 transcript from AS11. The exon 2 in the repeat is properly spliced. The alteration of the transcript thus does not disturb the reading frame. However, this additional exon 2 sequence in the AS11 transcript would result in an altered DGAT protein with the 27 amino acid insertion ¹³¹SHAGLFNLCVVVLI AVNSRLIENLMK¹⁵⁷ [SEQ ID NO:11]. The inventors' data shows that this insertion results in a 40-70% reduction
15 in DGAT activity throughout seed development (Katavic et al., 1995). The 81 bp insert responsible for reduced DGAT activity in AS11 is visible in the comparison of RT-PCR products (Figure 7b: Compare lane 5 (WT) and lane 6 (AS11).) The DNA aberration observed in the AS11 mutant was unexpected, since ethyl
methanesulfonate (EMS) generally causes point mutations. Although we cannot
20 rule out the possibility that this AS11 mutant was the result of a spontaneous mutation event, EMS-induced deletions and insertions have been reported in other systems (Mogami et al., 1986, Okagaki et al., 1991)

The TAG1 gene insertion in Arabidopsis mutant AS11 affects seed triacylglycerol accumulation, but not sterol ester accumulation in seeds.

25 Because TAG1 also showed some sequence homology to acyl CoA: cholesterol acyltransferases (ACATs) from a number of species (Chang et al., 1997), the inventors compared both triacylglycerol and sterol ester accumulation in seeds of the wild-type *A. thaliana* and AS11 mutant. While the triacylglycerol content and TAG/DAG ratios were reduced in AS11 (i.e. increased proportion of
30 seed oil DAGs,) in contrast, the proportions of sterol esters in WT and AS11 seeds were similar, at 0.8 and 1% of the total lipid extract, respectively (Table 1). If the

TAG1 lesion affected ACAT-like activity, one might expect a reduction in seed sterol esters, but this was not observed. These results indicated that *TAG1* is not involved in sterol-ester homeogenesis, and thus not an acyl CoA: sterol acyltransferase.

TAG1 expression in yeast.

- 5 The *TAG1* cDNA overexpressed in yeast resulted in a 3.5 to 4-fold increase in microsomal DGAT activity compared to plasmid only (*pYES2*) control transformants (Fig. 8), confirming that the *TAG1* gene product functions as a DGAT. When ¹⁴C18:1-CoA was added to the yeast lysates, sterol esters were also labeled *in vitro* (data not shown), but there was no significant difference in the ¹⁴C-labeled
- 10 sterol esters produced by lysates from the *pYES2* GAL-induced control and the *pYES2:TAG1* Gal-induced transformant. This confirms that the *TAG1* product does not encode an acyl-CoA: sterol acyltransferase (like ACAT).

Complementation of the A. thaliana AS11 Mutant Line by Transformation with the DGAT cDNA.

- 15 The cloned full-length DGAT cDNA was used as a template for PCR amplification with the primers DGATXbaI (CTAGTCTAGAATGGCGATTTTGGGA; SEQ IN NO: 12) and DGATXhoI (GCGCTCGAGTTTCATGACATCGA; SEQ ID NO:13) to provide new restriction sites on each end of the sequence as described in Experimental Procedures. A 1.6kb fragment was excised by a XbaI/KpnI digestion
- 20 and ligated into the corresponding sites of the pSE129 vector (provided by Dr. P. Covello, PBI/NRC). pSE129A is a vector derived from the plant transformation vector pRD400 (Datla et al. 1992). The vector pSE129A contains the seed-specific napin promoter and the nos terminator cloned into the EcoRI and HindIII sites of the pRD400 plasmid (Figure 9). Hence in the DGAT-pSE129A construct, the
- 25 *Arabidopsis* DGAT cDNA is under the control of the napin promoter. The construct integrity was confirmed by sequencing.

- The pSE129A containing the napin:DGATcDNA was introduced into *A. tumefaciens*, used to transform *A. thaliana* mutant AS11, and progeny analyzed as described in Experimental Procedures. A number of T₂ transgenic lines were
- 30 isolated which complemented the fatty acid mutant phenotype found in AS11 (reduced 20:1 and elevated polyunsaturated C₁₈s), restoring the wild-type seed fatty

acid profile (Figure 10). This finding confirms the nature of the lesion in AS11 and directly ties the AS11 lipid phenotype to this mutation.

Over-Expression of the DGAT cDNA in Wild-Type A. thaliana

The cloned full-length DGAT cDNA was used as a template for PCR
5 amplification with the primers DGATXbaI (CTAGTCTAGAATGGCGATTTTGGA; SEQ
ID NO:12) and DGATXhoI (GCGCTCGAGTTTCATGACATCGA; SEQ ID NO:13) to
provide new restriction sites on each end of the sequence as described in
Experimental Procedures. A 1.6kb fragment was excised by a XbaI/KpnI digestion
and ligated into the corresponding sites of the pSE129 vector (provided by Dr. P.
10 Covello, PBI/NRC). pSE129A is a vector derived from the plant transformation
vector pRD400 (Datla et al. 1992). The vector pSE129A contains the seed-specific
napin promoter and the nos terminator cloned into the EcoRI and HindIII sites of the
pRD400 plasmid (Figure 9). Hence in the DGAT-pSE129A construct, the
Arabidopsis DGAT cDNA is under the control of the napin promoter. The construct
15 integrity was confirmed by sequencing.

The pSE129A containing the napin:DGATcDNA was introduced into *A.*
tumefaciens, used to transform wild-type *A. thaliana*, and progeny analyzed as
described in Experimental Procedures. A number of T₂ transgenic lines were
isolated which exhibited an increased oil content (Figure 11) an increased average
20 100-seed weight (Figure 12) and a strong linear correlation between the two traits
(Figure 13).

In terms of fatty acyl composition, wild type lines containing over-expressed
DGAT cDNA showed a decrease in the total saturates, and increases in the
monounsaturates and in the 18:1/[18:2 + 18:3] index, as shown in Table 2 below.
25 Such changes are all towards a 'healthier' oil profile, and can be applied directly to
canola, other oilseeds in the *Brassicaceae* and other edible oil crops to produce
similar oil composition improvements.

Table 2

Fatty acid composition of seed oil from *A. thaliana* non-transformed wild-type controls (WT Con) and three T2 transgenic lines (2', 9 and 11) of wild type transformed with the DGAT cDNA under the control of a napin promoter (napin: DGAT).

Line	Total Saturates ^a Wt %	Monounsaturates ^b Wt %	18:1/[18:2 + 18:3] index ^c
WT Control	15.1 ± 0.1	36.7 ± 0.2	29.9 ± 0.6
2' napin:DGAT	13.4	38.6	34.1
9 napin:DGAT	13.1	39.3	35.6
11 napin:DGAT	13.1	38.3	33.0

^a Includes 16:0, 18:0, 20:0, 24:0

^b includes 18:1, 20:1, 22:1, 24:1

^c ([Wt % 18:1] + [Wt % 18:2 + Wt % 18:3]) × 100

EXPERIMENTAL PROCEDURES

Plant Material

- 5 *Arabidopsis thaliana* ecotype Columbia and mutant AS11 were grown under conditions described previously (Katavic et al., 1995). The *A. thaliana* mutant line AS11 was generated and characterized relative to wild type (WT) *A. thaliana* ecotype Columbia, as described by Katavic et al., (1995); (ATCC NO: PTA-1013).

DNA manipulation

- 10 Standard methods and procedures were used for DNA preparation, plasmid propagation and isolation (Sambrook et al., 1989). Sequencing was conducted on an Applied Biosystems Model 373A DNA Sequencing System using the *Taq* DyeDeoxy™ Terminator Cycle Sequencing Kit (Applied Biosystems, Inc.). The nucleotide and the deduced amino acid sequences were compared with sequences
15 available in databanks using the BLAST program (Altschul et al., 1990).

Southern and Northern analysis

Total RNA was extracted from different tissues at various developmental stages, using the method of Lindstrom and Vodkin (1991). RNA samples were denatured with formaldehyde and separated on 1.2% formaldehyde-agarose gels.

- 5 About 5 µg of total RNA was loaded, and the amount of RNA per lane was calibrated by the ethidium bromide-staining intensity of the rRNA bands. Genomic DNA was isolated, digested with restriction enzymes and a Southern blot analysis was performed according to Sambrook et al. (1989). The TAG1 DNA probe was ³²P labeled by random-priming according to protocols of the manufacture (BRL).

10 *PCR strategy*

Primers used for the amplification of the TAG1 gene were as follows:

DGAT1 (AGACACGAATCCCATTCACCGA; SEQ ID NO:14), DGAT2

(AGTGGTGACAACGCAGGGATGATG; SEQ ID NO:15), DGAT3 (ATGGTCGCTCCACATTGTGT;

SEQ ID NO:16), DGAT4 (CATACAATCCCATGACATTATCA; SEQ ID NO:17). DGAT1

- 15 and DGAT2 amplify the 5' half of the TAG1 gene and DGAT3 and DGAT4 amplify the 3' end of the TAG1 gene. Genomic DNA from AS11 was used as template for PCR amplification of the mutant TAG1 allele using the thermal profile: 94° C 3 min; 40 cycles of 94° C 30 seconds, 62° C 45 seconds, 72° C 1 min; and 72° C 15 min.

To further confirm the mutation, primers A (CGACCGTCGGTCCAGCTCATCGG; [SEQ ID

- 20 NO:18]) and B (GCGGCCAATCTCGCAGCGATCTTG; [SEQ ID NO:19]), as well as primers C

(TAAACAGTAGACTCATCATCG; [SEQ ID NO:20]) and B, were used in pairs, respectively,

to amplify the internal fragment containing the mutation. The primers DGAT1 and

DGAT4 were used for PCR amplification of the cDNA with an *A. thaliana* silique cDNA library as template. Primers A and B were also used in RT-PCR

- 25 amplification of the cDNA fragment encompassing the insertion segment.

Construction of TAG1 Multicopy Vector and Transformation and Characterization of DGAT Expression in Yeast

The TAG1 cDNA was cloned into pBluescript SK as described (Hadjeb and Berkowitz, 1996). The cDNA was cut out from the vector with KpnI/XbaI, and

- 30 subsequently cloned into the respective sites of the yeast expression vector pYes2 (Invitrogen). The construct was confirmed by sequencing. Constructs with TAG1

transcription under the control of the GAL1 promoter released a fragment of approximately 1.9 kb. Because the TAG1 fragment has its own initiating ATG codon, the product expressed is not a fusion protein. As a host for yeast expression, an SLC deletion strain (YMN5 [slc1 Δ 2::LEU2 ura3]) (kindly provided by M.M. Nagiec and R.C. Dickson, University of Kentucky, Lexington, KY; Nagiec et al., 1993) was used; we reasoned that in this mutant, the endogenous DAG pool may be lower than in WT yeast, and that this would allow us to maximize the activity from over-expressed TAG1 in the presence of exogenously supplied ^{14}C -DAG during in vitro DGAT assays of transformant lysates. Yeast transformation was performed according to Elble (1992). YMN5 transformants containing vector only (pYES2) were used as controls. Single colonies were cultured overnight in 20 mL of SD medium (Synthetic Dextrose medium with glucose and without uracil, as described by Ausubel et al., 1995, Vol. 2, p. 13.1.3) on a rotary shaker (270 rpm) at 28°C. Cells were pelleted from the overnight culture and resuspended in 50 mL of medium for induction of expression (SD medium containing galactose and without uracil). Cells were reincubated at 28°C, with shaking at 270 rpm, and harvested after 4-6 hr. GAL-induced yeast transformants were harvested by centrifugation at 5000 rpm for 5 min and resuspended in 100 mM Hepes-NaOH, pH 7.4, containing 1 mM EDTA and 1 mM DTT. Cell lysates were prepared using acid-washed glass beads as described by Ausubel et al. (1995). Protein in yeast lysates was measured using the Bradford (1976) assay, protein levels in each lysate were normalized and aliquots (250 μg protein) were assayed for DGAT activity as described below.

Lipid Substrates and DGAT Analyses

^{14}C -labeled diolein [1- ^{14}C oleic] (Sp. activity 55 mCi/ mmol) was purchased from American Radiolabeled Chemicals (St. Louis, MO). The ^{14}C -labelled *sn*-1,2-diolein isomer was purified by TLC on borate-impregnated plates and emulsified in Hepes buffer the presence of 0.2% Tween-20 as described by Taylor et al., (1991). 20:1-CoA, CoASH, ATP, and all other biochemicals were purchased from Sigma.

DGAT assays were conducted at pH 7.4, with shaking at 100 rpm in a water bath at 30°C for 30-60 min. Assay mixtures (0.5 mL final volume) contained lysate protein (250 μg), 90 mM Hepes-NaOH, 0.5 mM ATP, 0.5 mM CoASH, 1 mM MgCl_2 , 200 μM *sn*-1,2 diolein (sp. activity 2 nC/nmol) in 0.02% Tween 20, and 18 μM 20:1-

CoA as the acyl donor. The ^{14}C -labeled TAGs were isolated by TLC and quantified as described by Taylor et al (1991).

Further Lipid and Sterol Ester Analyses in AS11 and WT:

Total lipid extracts (TLEs), and lipid class analyses in WT and the AS11 mutant were performed as described by Taylor et al., (1991; 1992) and by Katavic et al., (1995). Relative seed oil content was also measured by magic angle sample spinning ^1H -NMR, according to the method of Rutar (1989). Analyses were conducted with 200-seed samples of intact wild-type and AS11 seeds using a Bruker AM wide-bore spectrometer (Bruker Analytische Masstechnik GHBH, Silberstreifen D-76287, Rheinstetten4/Karlsruhe, Germany) operating at 360 MHz. To reduce anisotropic line broadening, the seed sample was rotated at 1 kHz in a zirconium rotor oriented 54.7° to the magnetic field. The integration response for resonances attributable to liquid-like oil were summed and the value for AS11 seed was recorded relative to the response for the WT control seed sample, the latter set at a value of 1.00.

Sterol esters were purified from the TLEs by thin layer chromatography (TLC) on Silica H plates developed in hexane: diethyl ether: formic acid (80:20:2, v/v/v). After elution from the silica H with chloroform: methanol (2:1, v/v), the sterol esters were quantified by saponification followed by methylation of the resulting fatty acids with 3N methanolic-HCl. The fatty acid methyl esters (FAMES) were analyzed by GC as described previously (Taylor et al., 1991). The free sterols released by saponification were also analyzed by GC on a 30 m DB-5 column; GC temperature program : initial temp: 180°C , increasing at $10^\circ\text{C}/\text{min}$ to 300°C and held at this temperature for 15 min. The sterol ester content was reported as a % of the TLE; i.e. FAMES released from sterol esters calculated as proportion of the FAMES released by transmethylation of the total lipid extract (TLE).

Construction of Plant Transformation Vector Containing the Wild-Type DGAT gene for Over-Expression in WT A. thaliana and Complementation of the A. thaliana AS11 Mutant:

30

Two primers:

Gen 1 (GAGAGGATCCACGCTCACGACCCATTCTTCCCG; [SEQ ID NO:21]), and

Gen 2 (AAGAAGGATCCATCCCCAAAACGGGACCACCAA; [SEQ ID NO:22])

- 5 were synthesized according to sequences upstream and downstream of the TAG1 gene. These primers were used to PCR amplify a genomic fragment of 5.1 kb from wild-type *A. thaliana*. The PCR fragment was purified and digested with BamHI and inserted into the corresponding site in plasmid pRD400 (Datla et al. 1992) to generate the plant transformation vector DGATg-pRD400.

10 *Construction of DGAT cDNA Plant Transformation Vector for Seed-Specific Expression:*

- The cloned full-length DGAT cDNA was used as a template for PCR amplification with the primers DGATXbaI (CTAGTCTAGAATGGCGATTTTGA; SEQ ID NO:12) and DGATXhoI (GCGCTCGAGTTTCATGACATCGA; SEQ ID NO: 13) to
15 provide new restriction sites on each end of the sequence. The PCR profile was as follows: 94°C 1 min; 30 cycles of 94°C 30 seconds, 55°C 30 seconds, 72°C 1 min; and 72°C 5 min. The PCR product was then ligated into the PCR-2.1 vector (Invitrogen). A 1.6kb fragment was excised by a XbaI/KpnI digestion and ligated into the corresponding sites of the pSE129 vector (provided by Dr. P. Covello,
20 PBI/NRC). pSE129A is a vector derived from the plant transformation vector pRD400 (Datla et al. 1992). The vector pSE129A contains the seed-specific napin promoter and the nos terminator cloned into the EcoRI and HindIII sites of the pRD400 plasmid (See Figure 9). Hence in the DGAT-pSE129A construct, the *Arabidopsis* DGAT cDNA is under the control of the napin promoter. The construct
25 integrity was confirmed by sequencing.

Transformation of Agrobacterium with Plant DGAT Vector Constructs:

- Electrocompetent *Agrobacterium* cells, GV3101 (pMP90) strain, were prepared as follows: An *Agrobacterium* culture was grown 24 to 48 hrs in 2YT, and when the absorbance at 600 nm reached 0.5 to 0.7, the cells were chilled on ice
30 and pelleted by centrifugation (5,000 x g, 10 min in a GSA rotor at 4°C). The pellet was washed in 1, 0.5 and 0.02 volumes of cold 10% sterile glycerol and

resuspended in 0.01 volume of cold 10% glycerol. The electrocompetent cells were then frozen in liquid N₂ and stored at -70°C. The *Agrobacterium* cells were transformed by electroporation with 20-50 ng of transforming DNA (either DGATg-pRD400 or DGAT-pSE129A) according to the manufacturer's instructions, plated on
5 a selective medium (LB with 50 µg/mL kanamycin) and incubated overnight at 28°C. Single transformed cells were grown overnight (28°C, 225 r.p.m.) in 5 mL LB with 50 µg/mL Kanamycin and 25 µg/mL Gentamycin. DNA extraction and purification were performed with a Qiaprep Spin Miniprep kit (Qiagen). The fidelity of the construct was re-checked by DNA sequencing before plant transformation.

10 *Transformation of Arabidopsis thaliana:*

The transformation protocol was adapted from that described by Clough and Bent (1998). Seeds of *Arabidopsis thaliana* ecotype Columbia and mutant AS11 (Katavic *et al.*, 1995) were grown at 22°C under fluorescent illumination (120 µE·m⁻²·s⁻¹) in a 16 h light/8 hour dark regime. Typically, four to six plants were raised in a
15 10 cm² pot in moistened Terra-lite Redi-earth (W. R. Grace & Co. Canada Ltd. Ajax, ON, Canada). To prevent the soil mix in the pot from falling into the inoculation media, soil was mounded as a platform with seeds sown on top, and the whole pot covered by a nylon window screen and secured by a rubber band. Plants were vacuum infiltrated in an *Agrobacterium* suspension when the first flowers started
20 opening.

To grow *Agrobacterium*, a 5 mL suspension in LB medium containing 50 µg/mL kanamycin and 25 µg/mL gentamycin was cultured overnight at 28°C. The day before infiltration, this "seed culture" was divided into four flasks containing 250 mL of LB medium supplemented with 50 µg/mL kanamycin and 25 µg/mL
25 gentamycin. These culture were grown overnight at 28°C. The next morning after the absorbance at 600 nm was checked (approximately = 1.0), the cells were harvested by centrifugation (5,000 x g, 10 min in a GSA rotor at room temperature) and resuspended in the infiltration medium (sucrose 5%; Silwet-77 0.005% in water) to obtain an optical density at 600 nm of 0.8. The *Agrobacterium* suspension was
30 then poured into a beaker and the potted plants inverted into the beaker so that the flowers and bolts were submerged. The beaker was then placed into a large Bell jar and a vacuum drawn using a vacuum pump, until bubbles formed on the stem

surfaces and the solution started to bubble slightly, and then the vacuum was released rapidly. [Note: The necessary time and pressure will vary from one lab setup to the next, but good infiltration is visibly apparent as uniformly darkened, water-soaked tissue.] Pots were removed from the beaker, laid on their side in a plastic tray and covered with a plastic dome, to maintain humidity. The following day, the plants were uncovered, set upright and allowed to grow for approximately four weeks in a growth chamber under continuous light conditions as described by Katavic et al., (1995). When the siliques were mature and dry, seeds were harvested and selected for positive transformants.

10 *Selection of Putative Transformants (Transgenic plants) and Analysis of Transgenic Plants:*

For each construct, seeds were harvested in bulk. Seeds were surface-sterilized by submerging them in a solution containing 20% bleach and 0.01% Triton X-100 for 20 min, followed by three rinses with sterile water. Sterilized seeds were then plated by resuspending them in sterile 0.1% phytagar at room temperature (about 1 mL phytagar for every 500-1000 seeds), and then applying a volume containing 2,000-4,000 seeds onto 150 x 15 mm kanamycin selection plate. Plates were incubated for 2 days in the cold without light, and then grown for 7-10 days in a controlled environment (22°C under fluorescent illumination ($120 \mu\text{E}\cdot\text{m}^{-2}\cdot\text{s}^{-1}$) in a 16 h light/8 hour dark regime). The selection media contain ½ MSG medium, 0.8% phytagar, 3% sucrose, 50ug/mL kanamycin and 50ug/ mL Timentin. Petri dishes and lids were sealed with a Micropore™ surgical tape tape (3M Canada, London, ON, Canada). After 7-10 days, drug-resistant plants that had green leaves and well established roots within the medium were identified as transformants and at the 3-5 leaf stage, selected transformants were transplanted into flats filled with heavily moistened soil mix. Transformants were grown to maturity and mature seeds (T_2 generation as defined in Katavic et al., (1994)) were harvested from individual plants, and further analyzed.

DNA isolation from and analysis of Transformants

30 Genomic DNA was isolated from individual T_1 plants following the protocol of Dellaporta et al., (1983). A PCR amplification using the paired primers described previously for the DGAT cDNA or for the DGAT gene, was performed to confirm the

presence of the cDNA or the gene, respectively, in the T₁ transformants. Southern analyses (Southern, 1975) were performed to select the transformants containing a single copy of the inserted fragment. DNA samples were digested with restriction enzymes (Bgl II for the DGAT cDNA and Eco RI for the DGAT gene), resolved by
5 electrophoresis on a 1% agarose gel, and Southern blotting performed using a nylon filter (Hybond-N+, Amersham) according to Sambrook *et al.* (1989). The DGAT cDNA fragment, labelled with α -[³²P] dCTP (NEN/DuPont) using the Random Primer DNA labelling kit (Gibco BRL), was used as a probe. Hybridization was performed at 60°C according to Church and Gilbert (1984). The filter was then
10 exposed to Kodak X-OMAT-AR film.

DEPOSIT INFORMATION

The following biological material has been deposited at the American Type Culture Collection (ATCC) of 10801 University Boulevard, Manassas, Virginia, 20110-2209, U.S.A. All of these deposits were made on behalf of the
15 Applicant/Assignee (National Research Council of Canada) under the terms of the Budapest Treaty on the dates indicated, and have been given the accession numbers shown below.

	Deposited Material	Date of Deposit	Accession No.
	Arabidopsis DGAT gene	November 29, 1999	PTA-988
20	Arabidopsis DGAT cDNA	November 29, 1999	PTA-989
	Arabidopsis ASII seeds	December 3, 1999	PTA-1013

The deposit receipts are shown later in this description.

25 SEQUENCE LISTING FREE TEXT

The Sequence Listing provided below contains free text entries in respect of SEQ ID NOs: 12 to 22. The free text used in the Sequence Listing is repeated as follows:

	SEQ ID NO:12	Primer of DGATXbaI
30	SEQ ID NO:13	Primer of DGATXhoI

	SEQ ID NO:14	Primer DGAT1
	SEQ ID NO:15	Primer DGAT2
	SEQ ID NO:16	Primer DGAT3
	SEQ ID NO:17	Primer DGAT 4
5	SEQ ID NO:18	Primer A
	SEQ ID NO:19	Primer B
	SEQ ID NO:20	Primer C
	SEQ ID NO:21	Primer Gen 1
	SEQ ID NO:22	Primer Gen 2.

10

A summary of all of the listed sequences is provided below for ease of review:

SEQ ID NO:1 - (pDGAT; vector containing isolated and purified deoxyribonucleic acid cDNA; ATCC No PTA-989), Genbank/EMBL Accession No. AJ238008.

- 15 SEQ ID NO:2 - The deduced amino acid sequence of the *Arabidopsis* DGAT (AtTAG1) protein.

SEQ ID NO:3 - (pgenomic DGAT; vector containing isolated and purified genomic deoxyribonucleic acid (genomic DNA) ATCC No PTA-988).

- 20 SEQ ID NO:4 - MDGAT, mouse DGAT [GenBank/EMBL Accession No. AF078752 (Cases *et al.*, 1998)].

SEQ ID NO:5 - HARGP1, human ARGP1 protein [GenBank/EMBL Accession No. AF059202; Oelkers *et al.*, 1998].

SEQ NO:6 - *Arabidopsis thaliana* expressed sequence tag (EST) [accession no. AA042298).

- 25 SEQ ID NO:7 - A diacylglycerol/phorbol ester-binding motif found in SEQ ID NO:2, SEQ ID NO:8 and SEQ ID NO:9 (⁴¹⁴HKWMVRHIYFP⁴²⁴).

SEQ ID NO:8 - *B. napus* DGAT amino acid sequence GenBank EMBL Accession No AF155224.

SEQ ID NO:9 - *B. napus* DGAT amino acid sequence GenBank/EMBL Accession No. AF164434.

5 SEQ ID NO: 10 - Targeting motif typical of members of the SnRK1 protein kinase family found in SEQ ID NO:2, SEQ ID NO:8 and SEQ ID NO:9 X-L²⁰⁰-X-K²⁰²-X-X-S²⁰⁵-X-X-X-V²⁰⁹

SEQ ID NO:11 - A 27 amino acid insertion repeat in SEQ ID NO:2 found in the *Arabidopsis thaliana* AS11 mutant.

¹³¹SHAGLFNLCVVLIHAVNSRLIENLMK¹⁵⁷

10 SEQ IN NO: 12 - CTAGTCTAGAATGGCGATTTTGGGA (nucleotide sequence of Primer DGATXbal).

SEQ ID NO:13 - GCGCTCGAGTTTCATGACATCGA (nucleotide sequence of Primer DGATXhol).

SEQ ID NO:14 - AGACACGAATCCCATTCCCACCGA (nucleotide sequence of Primer DGAT1).

15 SEQ ID NO:15 - AGTGGTGACAACGCAGGGATGATG (nucleotide sequence of Primer DGAT2).

SEQ ID NO:16 - ATGGTCGCTCCCACATTGTGT (nucleotide sequence of Primer DGAT3).

20 SEQ ID NO:17 - CATACAATCCCCATGACATTTATCA (nucleotide sequence of Primer DGAT4).

SEQ ID NO:18 - CGACCGTCGGTCCAGCTCATCGG (nucleotide sequence of Primer A).

SEQ ID NO:19 - GCGGCCAATCTCGCAGCGATCTTG (nucleotide sequence of Primer B).

25 SEQ ID NO:20 - TAAACAGTAGACTCATCATCG (nucleotide sequence of Primer C).

SEQ ID NO:21 - GAGAGGATCCACGCTCACGACCCATTCTTCCCG (nucleotide sequence of primer Gen 1).

SEQ ID NO:22 - AAGAAGGATCCATCCCCAAAACGGGACCACCAA
(nucleotide sequence of primer Gen 2).

5 SEQ ID NO:23 - AS11 mutant DGAT cDNA nucleotide sequence.

SEQ ID NO:24 - AS11 mutant DGAT genomic DNA nucleotide sequence.

SEQ ID NO:25 - the deduced amino acid sequence of SEQ ID NO:23.

ATCC

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BUDAPEST TREATY ON THE INTERNATIONAL RECOGNITION OF THE DEPOSIT OF MICROORGANISMS FOR THE PURPOSES OF PATENT PROCEDURE

INTERNATIONAL FORM

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To: (Name and Address of Depositor or Attorney)

NRC Canada
Attn: David C. Taylor
Plant Biotechnology Institute
110 Gymnasium Place
Saskatoon, SK S7N 0W9 Canada

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Deposited on Behalf of: National Research Council of Canada

Identification Reference by Depositor:

Patent Deposit Designation

Arabidopsis DGAT gene
Arabidopsis DGAT cDNA

PTA-988
PTA-989

The deposits were accompanied by: ___ a scientific description ☒ a proposed taxonomic description indicated above. The deposits were received November 29, 1999 by this International Depository Authority and have been accepted.

AT YOUR REQUEST: ☒ We will not inform you of requests for the strains.

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Signature of person having authority to represent ATCC:


Barbara M. Halley, Administrator, Patent Depository

Date: December 3, 1999

cc: Kirby, Eades, Gale and Baker

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THE DEPOSIT OF MICROORGANISMS FOR THE PURPOSES OF PATENT PROCEDURE****INTERNATIONAL FORM****RECEIPT IN THE CASE OF AN ORIGINAL DEPOSIT ISSUED PURSUANT TO RULE 7.3
AND VIABILITY STATEMENT ISSUED PURSUANT TO RULE 10.2****To: (Name and Address of Depositor or Attorney)**

National Research Council of Canada
Attn: David C. Taylor
Plant Biotechnology Institute
110 Gymnasium Place
Saskatoon, SK S7N 0W9
Canada

Deposited on Behalf of: National Research Council of Canada**Identification Reference by Depositor:****Patent Deposit Designation***Arabidopsis* AS11

PTA-1013

The seeds were accompanied by: a scientific description ☒ a proposed taxonomic description indicated above.
The seeds were received December 3, 1999 by this International Depository Authority and have been accepted.

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If the seeds should die or be destroyed during the effective term of the deposit, it shall be your responsibility to replace them with viable seeds of the same.

The seeds will be maintained for a period of at least 30 years from date of deposit, or five years after the most recent request for a sample, whichever is longer. The United States and many other countries are signatory to the Budapest Treaty.

The viability of the seeds cited above was tested December 23, 1999. On that date, the seeds were viable.

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Signature of person having authority to represent ATCC:

Barbara M. Hailey
Barbara M. Hailey, Administrator, Patent Depository

Date: January 3, 2000

cc: Kirby, Eades et al.

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The teachings of the above references are hereby incorporated by reference.

CLAIMS:

1. Isolated and purified deoxyribonucleic acid (DNA), characterized in that said DNA includes a sequence according to SEQ ID NO:1 or a part of SEQ ID NO:1, or a sequence that is substantially homologous to SEQ ID NO:1.
2. Isolated and purified deoxyribonucleic acid (DNA), characterized in that said DNA includes a sequence according to SEQ ID NO:3 or a part of SEQ ID NO:3, or a sequence that is substantially homologous to SEQ ID NO:3.
3. A vector for transformation of plant cells, characterized in that said vector contains a deoxyribonucleic acid sequence according to SEQ ID NO:1, or a part of SEQ ID NO:1, or a sequence that is substantially homologous to SEQ ID NO:1.
4. A vector for transformation of plant cells, characterized in that said vector contains a deoxyribonucleic acid sequence according to SEQ ID NO:3, or a part of SEQ ID NO:3, or a sequence that is substantially homologous to SEQ ID NO:3.
5. A vector for transformation of plant cells, characterized in that said vector contains a deoxyribonucleic acid sequence according to SEQ ID NO:23, which is SEQ ID NO: 1 altered to contain an 81 bp insertion, such that the deduced amino acid sequence of the encoded protein contains the repeated sequence SHAGLFNLCVVVLIAVNSRLIIENLMK according to SEQ ID NO:25, where the spacing and identity of the underlined amino acids are identical or are replaced by conserved substitutions.
6. A vector according to claim 3 or claim 5, characterized in that said sequence is present in said vector in a sense orientation.
7. A vector according to claim 3, characterized in that said sequence is present in said vector in an anti-sense orientation.
8. Plasmid pDGATcDNA (ATCC PTA-989).
9. Plasmid pDGATgene (ATCC PTA-988).

10. A plant having a genome, characterized in that the genome contains an introduced nucleotide sequence of SEQ ID NO:1, or a part of SEQ ID NO:1, or a sequence that is substantially homologous to SEQ ID NO:1.

11. A plant seed having a genome, characterized in that said genome contains an introduced nucleotide sequence of SEQ ID NO:1, or a part of SEQ ID NO:1, or a sequence that is substantially homologous to SEQ ID NO:1.

12. A genetically transformed plant, characterized in that said genome has been transformed by a vector according to claim 3 or claim 4 or claim 5.

13. A genetically transformed plant seed, characterized in that said seed has been transformed by a vector according to claim 3 or claim 4 or claim 5.

14. A plant seed as claimed in Claim 11 or Claim 13, characterized by exhibiting an altered seed oil content compared to an average of a statistically-significant number of seeds of genomically-unmodified plants of the same genotype grown in identical conditions at the same time.

15. A plant seed as claimed in Claim 11 or Claim 13, characterized by exhibiting an altered diacylglycerol content in its seed oil compared to an average of a statistically-significant number of seeds of genomically-unmodified plants of the same genotype grown in identical conditions at the same time.

16. A plant seed as claimed in 11 or 13, characterized by exhibiting a seed oil with an altered fatty acyl composition compared to an average of a statistically-significant number of seeds of a genomically-unmodified plant of the same genotype grown in identical conditions at the same time.

17. A plant as claimed in 10 or 12, characterized by exhibiting an enhanced biomass compared to an average of a statistically-significant number of genomically-unmodified plants of the same genotype grown in identical conditions at the same time.

18. A seed as claimed in 11 or 13, characterized by exhibiting an enhanced biomass compared to an average of a statistically-significant number of seeds of genomically-unmodified plants of the same genotype grown under identical conditions at the same time.

19. A method of producing transgenic plants by introducing a nucleotide sequence into a genome of said plant, characterized in that said nucleotide sequence introduced into said genome includes SEQ ID NO:1 or SEQ ID NO:3, or a part of SEQ ID NO:1 or SEQ ID NO:3, or a sequence that is substantially homologous to SEQ ID NO:1, or to SEQ ID NO:3, or to or SEQ ID NO: 1, or a part of SEQ ID NO:1 or SEQ ID NO:3, or a sequence that is substantially homologous to SEQ ID NO:1 or SEQ ID NO:3 or SEQ ID NO:1 containing an 81 bp insertion [SEQ ID NO:23] such that the deduced amino acid sequence of the encoded protein contains the repeated sequence SHAGLFNLCVVVLIAVNSRLIIENLMK according to SED ID NO:25, where the spacing and identity of the underlined amino acids are identical or are replaced by conserved substitutions.

20. A method according to claim 19, characterized in that said plant is a member of the Brassicaceae.

21. A method according to claim 19, characterized in that said plant is selected from the group consisting of *Arabidopsis thaliana*, borage (*Borago* spp.), Canola, castor (*Ricinus communis*), cocoa bean (*Theobroma cacao*), corn (*Zea mays*), cotton (*Gossypium* spp), *Crambe* spp., *Cuphea* spp., flax (*Linum* spp.), *Lesquerella* and *Limnanthes* spp., Linola, nasturtium (*Tropaeolum* spp.), *Oenothera* spp., olive (*Olea* spp.), palm (*Elaeis* spp.), peanut (*Arachis* spp.), rapeseed, safflower (*Carthamus* spp.), soybean (*Glycine* and *Soja* spp.), sunflower (*Helianthus* spp.), tobacco (*Nicotiana* spp.), *Vernonia* spp., wheat (*Triticum* spp.), barley (*Hordeum* spp.), rice (*Oryza* spp.), oat (*Avena* spp.) sorghum (*Sorghum* spp.), rye (*Secale* spp.) and other members of the *Gramineae*.

22. A plant DNA sequence or part thereof, characterized in that the sequence is substantially homologous to at least a part of SEQ ID NO:1 or SEQ ID NO:3, and in that said sequence has been isolated, characterized or designed using sequence information from SEQ ID NO:1 or SEQ ID NO:3, or SEQ ID NO:1 containing an 81 bp insertion [SEQ ID NO:23] such that the deduced amino acid sequence of the encoded protein contains the repeated sequence SHAGLFNLCVVVLIAVNSRLIIENLMK according to SED ID NO:25, where the spacing and identity of the underlined amino acids are identical or are replaced by conserved substitutions.

23. A method of changing the oil content, acyl composition or diacylglycerol/triacylglycerol proportions of the seed oil of plant seeds by introducing a sense or anti-sense nucleic acid construct into a plant transformation vector, using the vector to transform the genome of a plant or plant seed, and then growing the plant or plant seed and extracting the oil from the plant seed, characterized in that said nucleic acid sequence is SEQ ID NO:1 or SEQ ID NO:3, or a part of SEQ ID NO:1 or SEQ ID NO:3, or a sequence that is substantially homologous to SEQ ID NO:1 or SEQ ID NO:3 or SEQ ID NO:1 [SEQ ID NO:23] containing an 81 bp insertion such that the deduced amino acid sequence of the encoded protein contains the repeated sequence SHAGLFNLCVVVLIAVNSRLIIENLMK according to SEQ ID NO:25, where the spacing and identity of the underlined amino acids are identical or are replaced by conserved substitutions.

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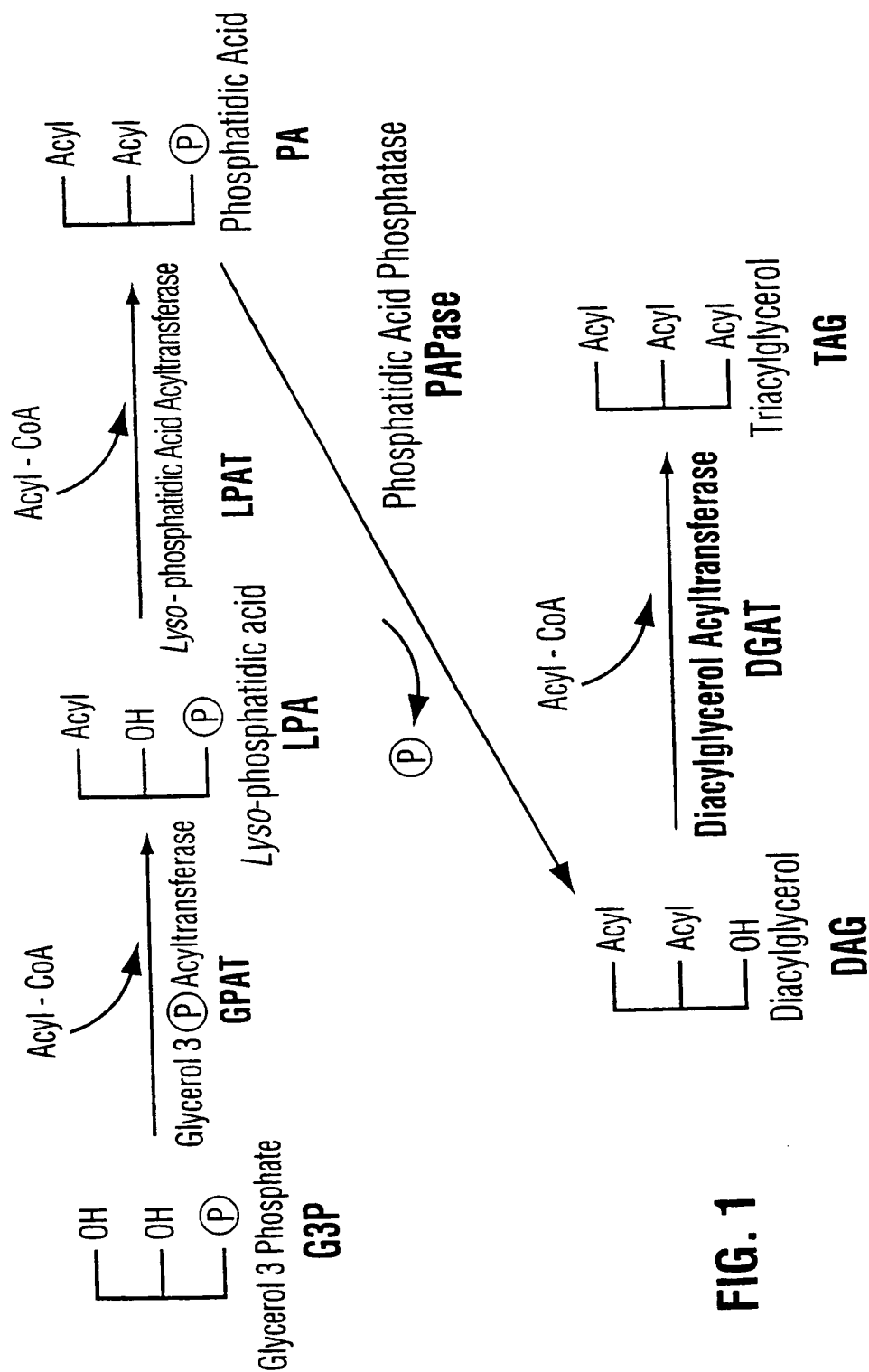


FIG. 1

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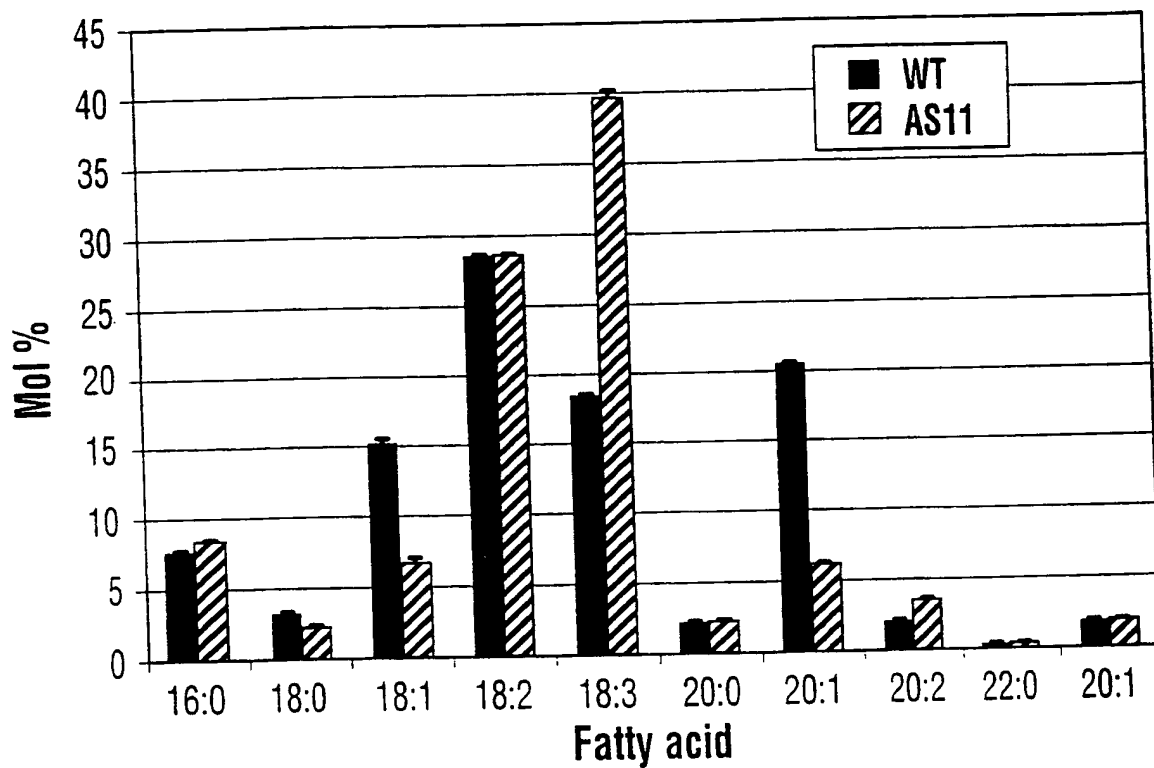


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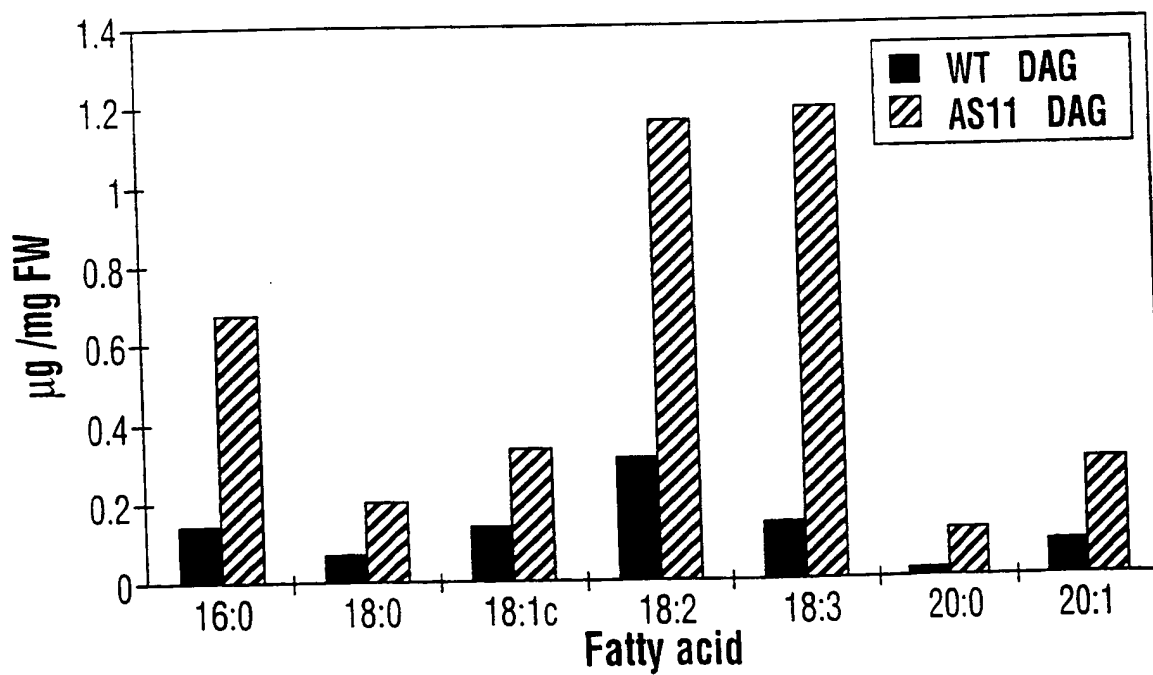
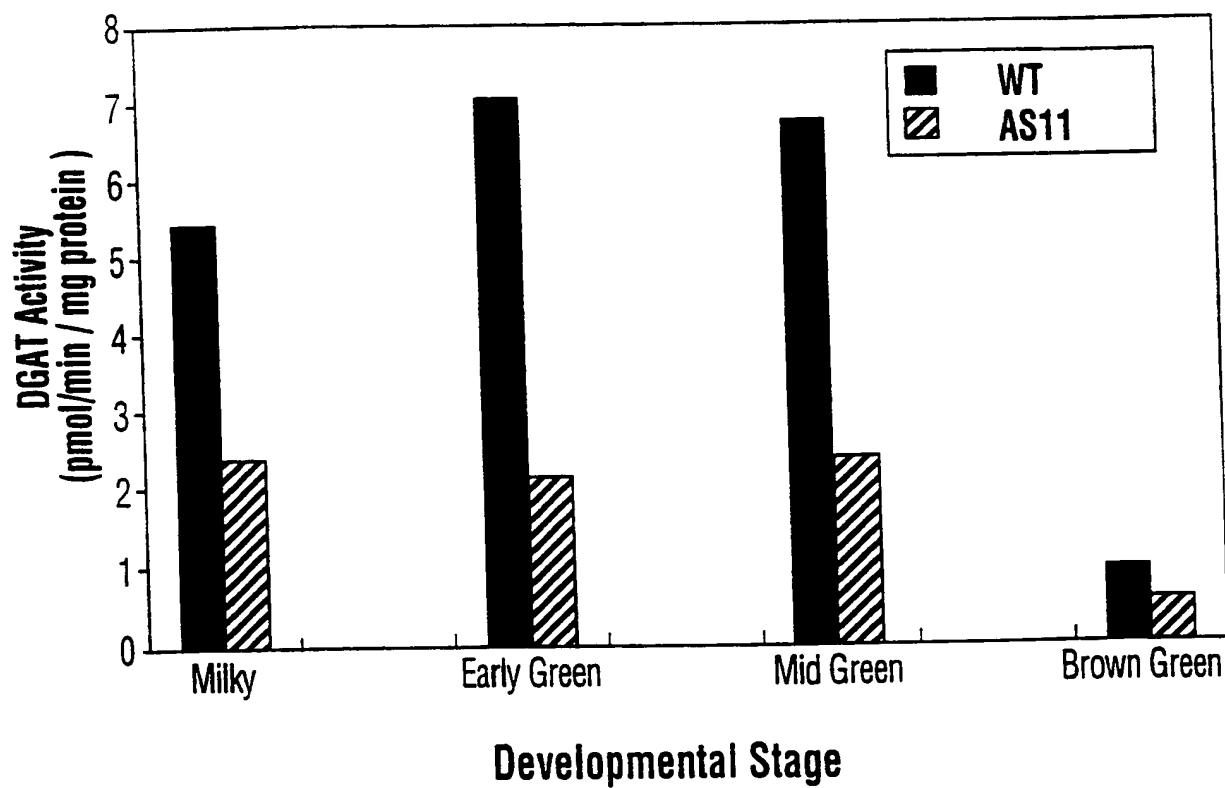


FIG. 3

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**FIG. 4**

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FIG. 5(a)

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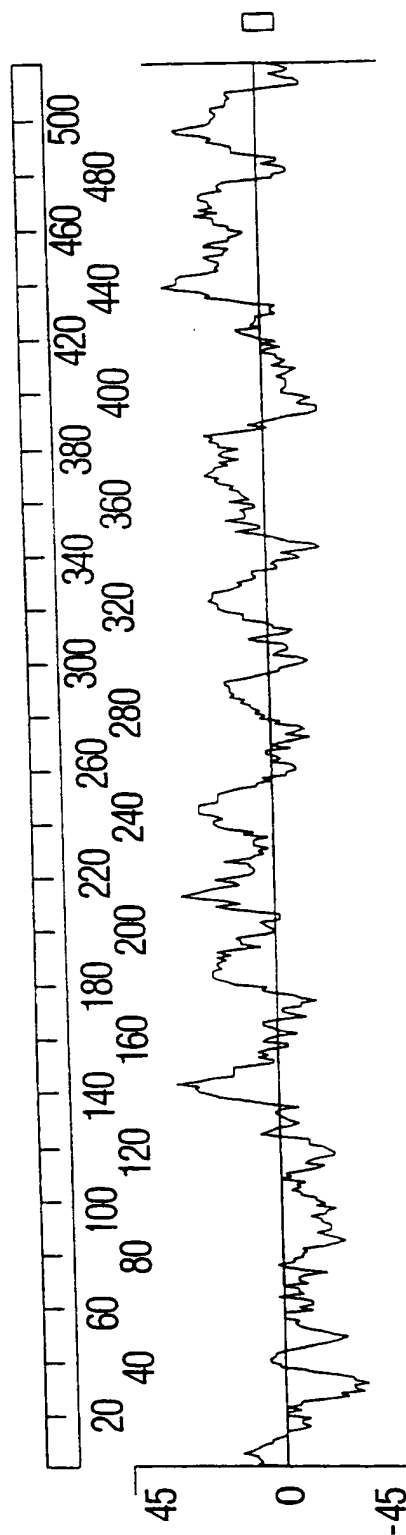


FIG. 5(b)

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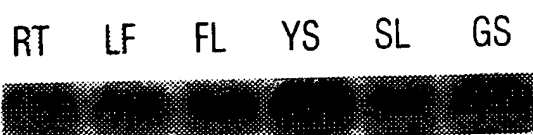


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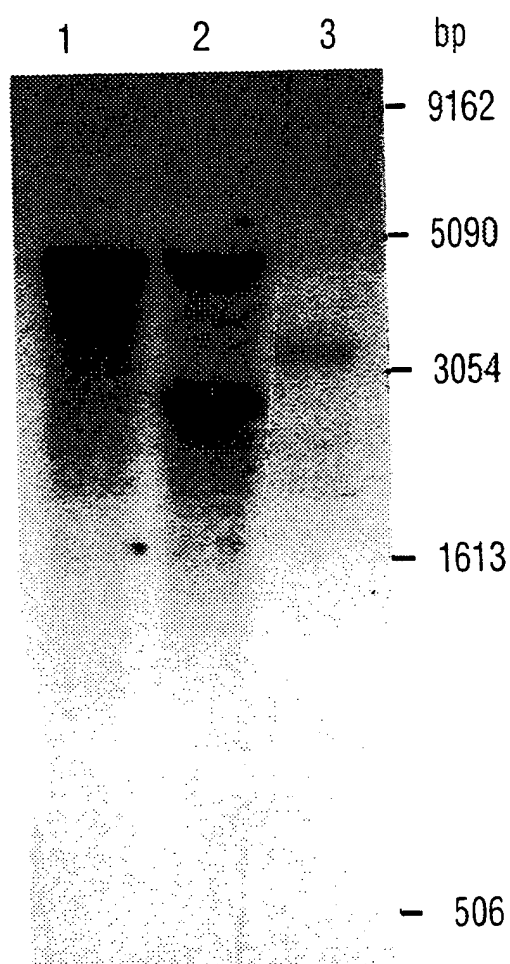


FIG. 6(b)

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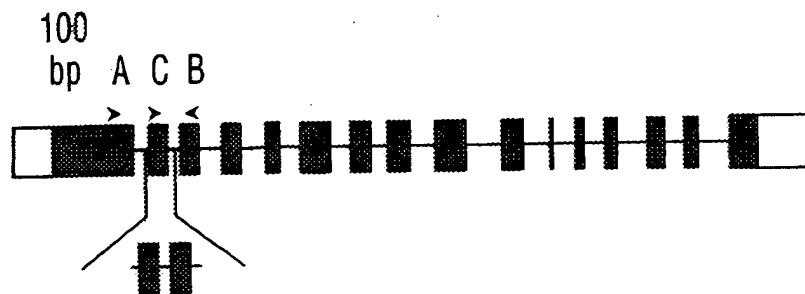


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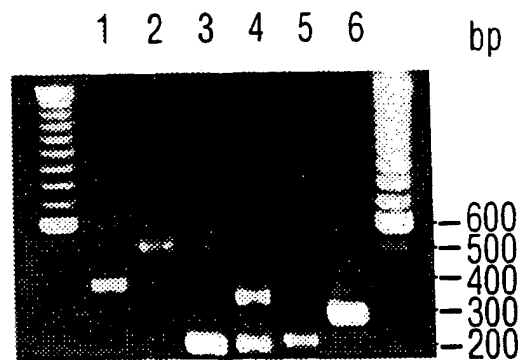


FIG. 7(b)

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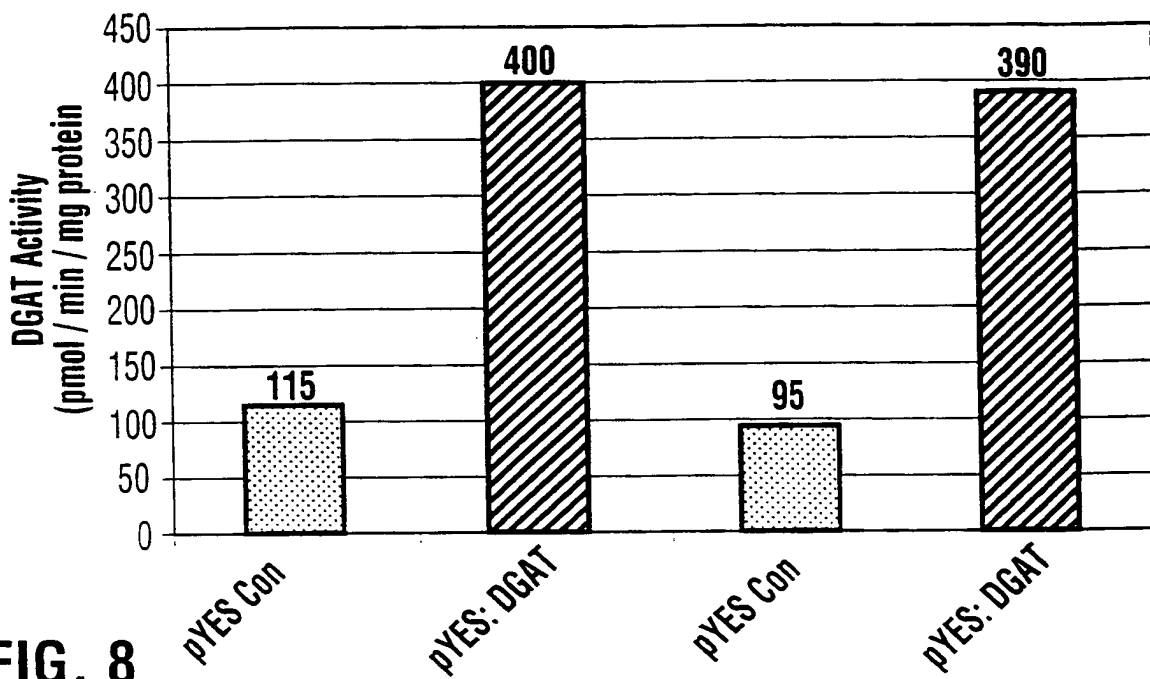


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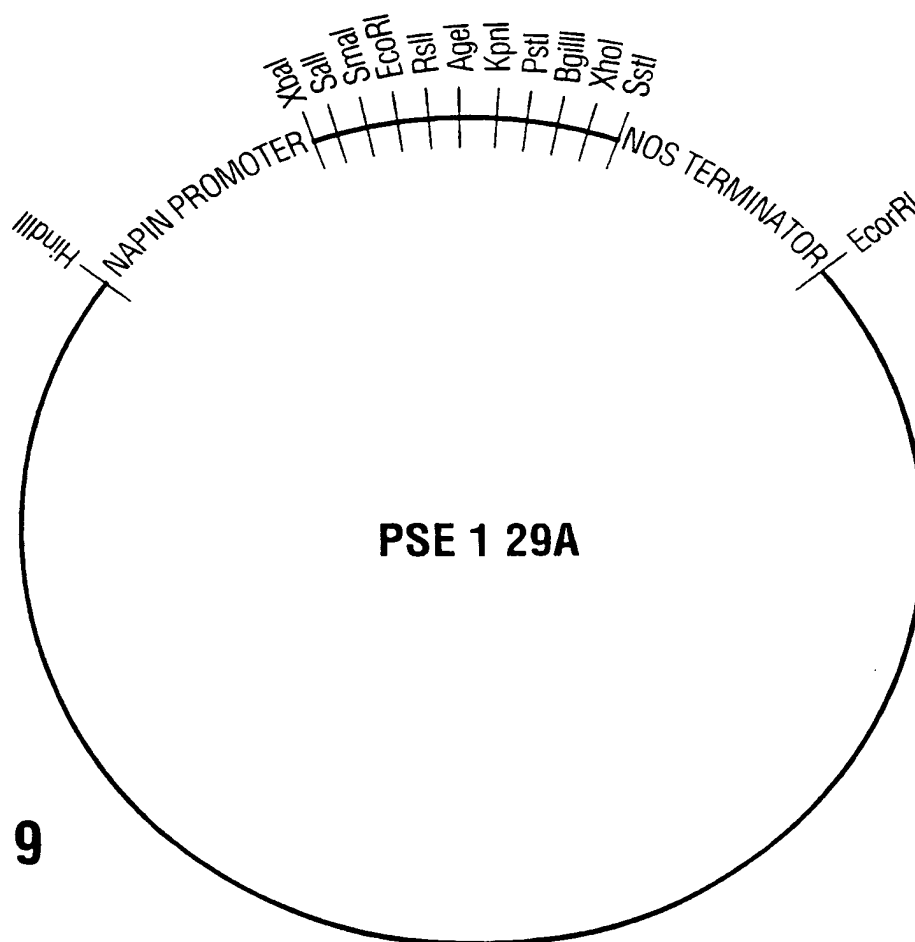


FIG. 9

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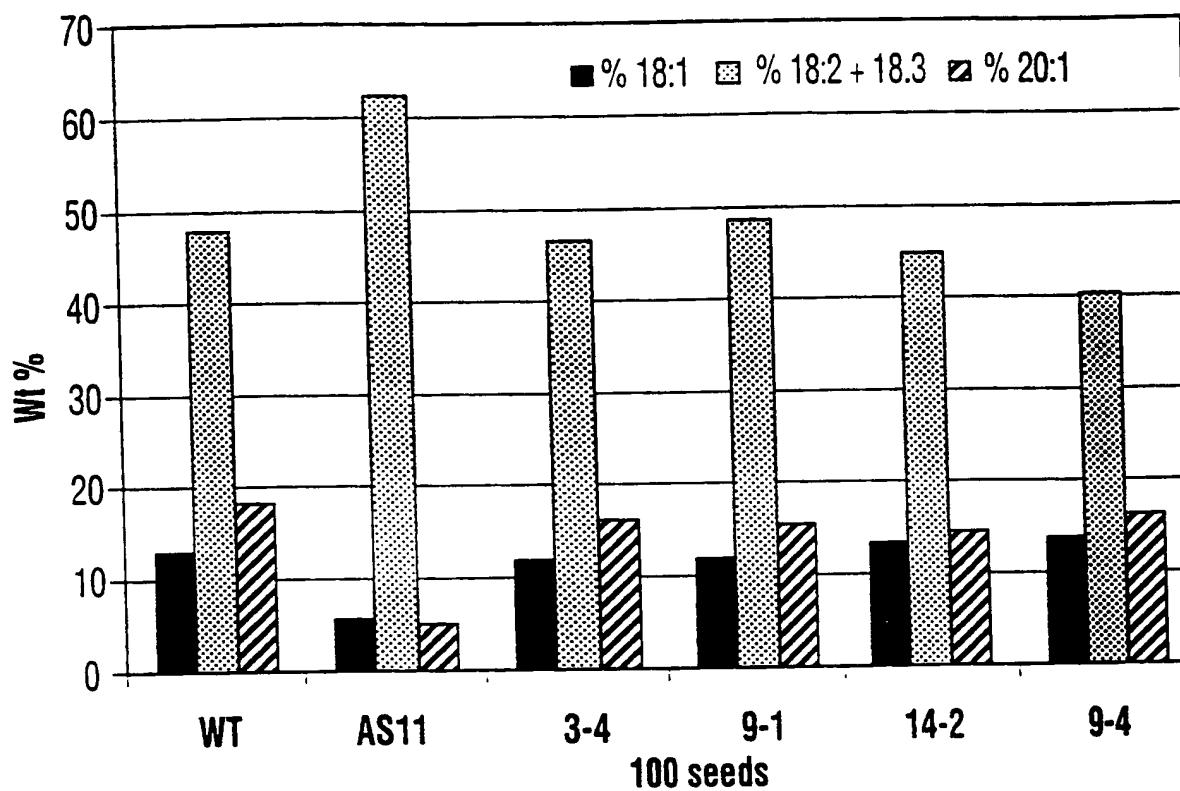


FIG. 10

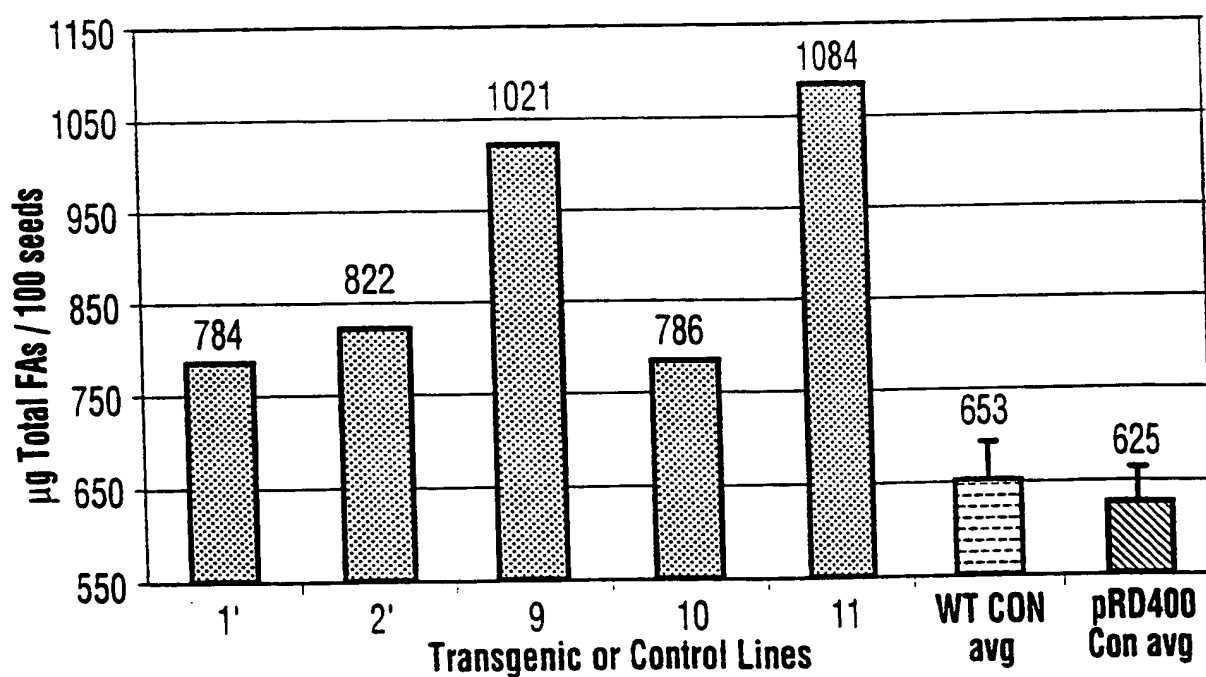


FIG. 11

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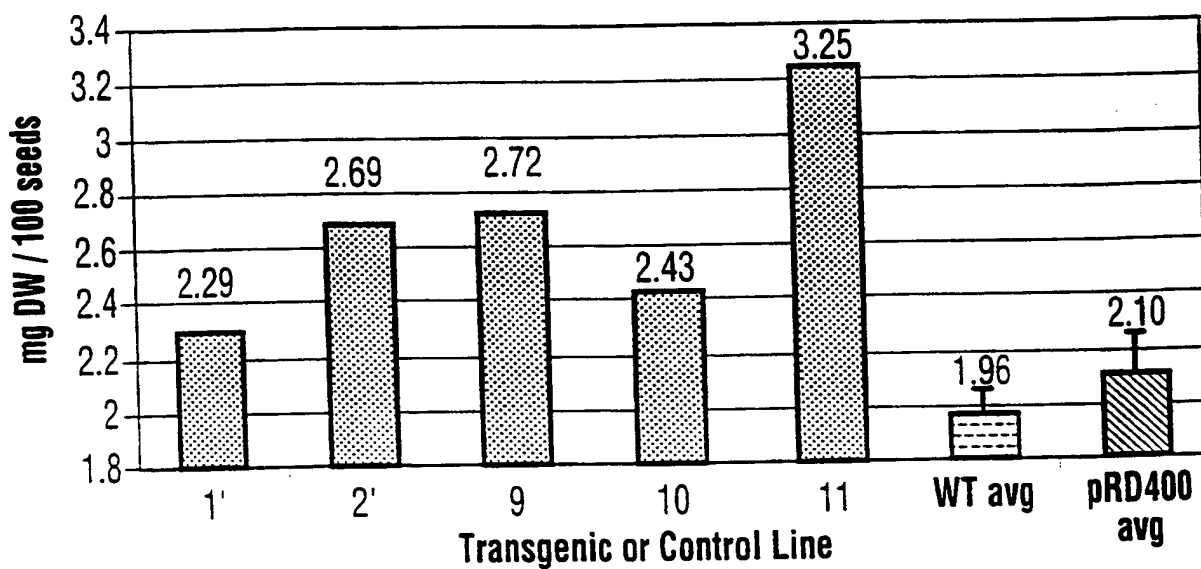


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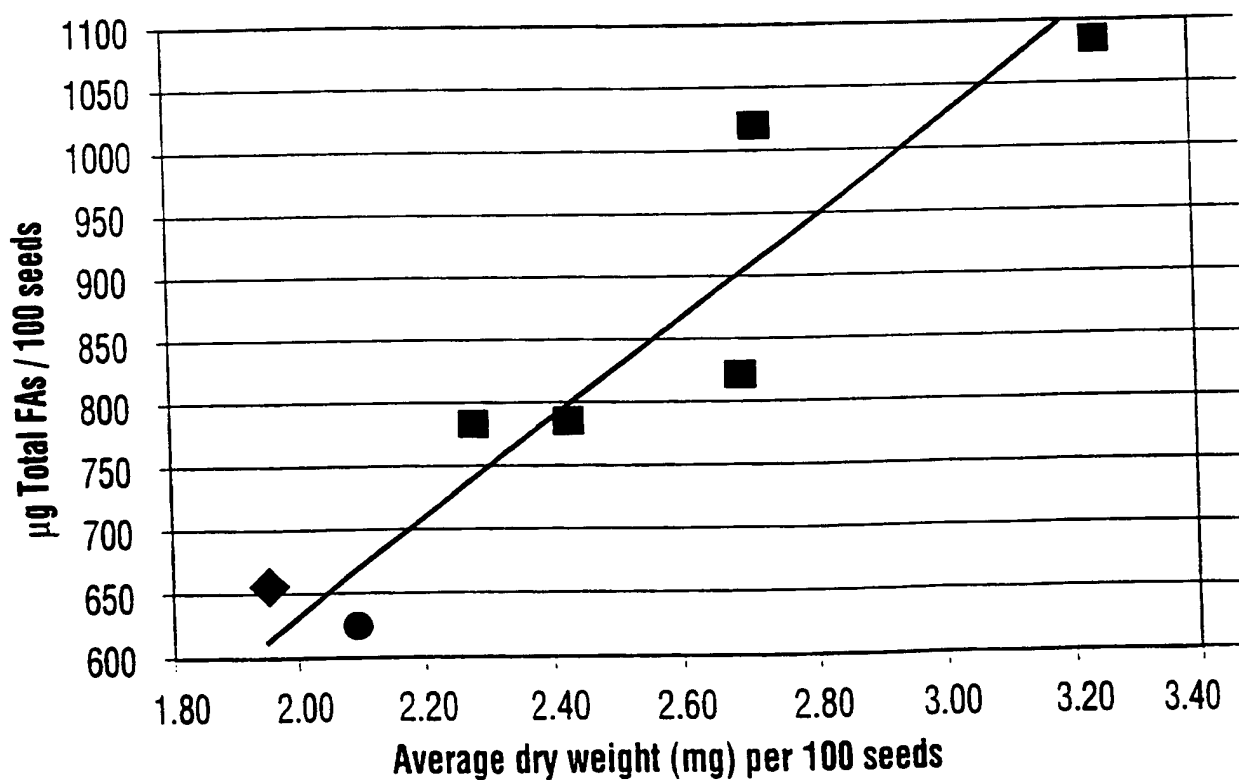


FIG. 13

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 Ser Tyr Ser Ile Met Phe Leu Lys Leu Tyr Ser Tyr Arg Asp Val Asn
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 Leu Trp Cys Arg Gln Arg Arg Val Lys Ala Lys Ala Val Ser Thr Gly
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 Lys Lys Val Ser Gly Ala Ala Ala Gln Gln Ala Val Ser Tyr Pro Asp
 245 250 255
 Asn Leu Thr Tyr Arg Asp Leu Tyr Tyr Phe Ile Phe Ala Pro Thr Leu
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 Cys Tyr Glu Leu Asn Phe Pro Arg Ser Pro Arg Ile Arg Lys Arg Phe
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 290 295 300
 Gly Leu Ile Gln Gln Trp Met Val Pro Thr Ile Gln Asn Ser Met Lys
 305 310 315 320
 Pro Phe Lys Asp Met Asp Tyr Ser Arg Ile Ile Glu Arg Leu Leu Lys
 325 330 335
 Leu Ala Val Pro Asn His Leu Ile Trp Leu Ile Phe Phe Tyr Trp Phe
 340 345 350
 Phe His Ser Cys Leu Asn Ala Val Ala Glu Leu Leu Gln Phe Gly Asp
 355 360 365

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Arg Glu Phe Tyr Arg Asp Trp Trp Asn Ala Glu Ser Val Thr Tyr Phe
 370 375 380

Trp Gln Asn Trp Asn Ile Pro Val His Lys Trp Cys Ile Arg His Phe
 385 390 395 400

Tyr Lys Pro Met Leu Arg His Gly Ser Ser Lys Trp Val Ala Arg Thr
 405 410 415

Gly Val Phe Leu Thr Ser Ala Phe Phe His Glu Tyr Leu Val Ser Val
 420 425 430

Pro Leu Arg Met Phe Arg Leu Trp Ala Phe Thr Ala Met Met Ala Gln
 435 440 445

Val Pro Leu Ala Trp Ile Val Gly Arg Phe Phe Gln Gly Asn Tyr Gly
 450 455 460

Asn Ala Ala Val Trp Val Thr Leu Ile Ile Gly Gln Pro Val Ala Val
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Leu Met Tyr Val His Asp Tyr Tyr Val Leu Asn Tyr Asp Ala Pro Val
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Gly Val

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 <213> human

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Asp Ala Ala Ala Gly Pro Asp Val Gly Ala Ala Gly Asp Ala Pro Ala
 35 40 45

Pro Ala Pro Asn Lys Asp Gly Asp Ala Gly Val Gly Ser Gly His Trp
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Glu Leu Arg Cys His Arg Leu Gln Asp Ser Leu Phe Ser Ser Asp Ser
 65 70 75 80

Gly Phe Ser Asn Tyr Arg Gly Ile Leu Asn Trp Cys Val Val Met Leu
 85 90 95

Ile Leu Ser Asn Ala Arg Leu Phe Leu Glu Asn Leu Ile Lys Tyr Gly
 100 105 110

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Ile Leu Val Asp Pro Ile Gln Val Val Ser Leu Phe Leu Lys Asp Pro
 115 120 125
 His Ser Trp Pro Ala Pro Cys Leu Val Ile Ala Ala Asn Val Phe Ala
 130 135 140
 Val Ala Ala Phe Gln Val Glu Lys Arg Leu Ala Val Gly Ala Leu Thr
 145 150 155 160
 Glu Gln Ala Gly Leu Leu Leu His Val Ala Asn Leu Ala Thr Ile Leu
 165 170 175
 Cys Phe Pro Ala Ala Val Val Leu Leu Val Glu Ser Ile Thr Pro Val
 180 185 190
 Gly Ser Leu Leu Ala Leu Met Ala His Thr Ile Leu Phe Leu Lys Leu
 195 200 205
 Phe Ser Tyr Arg Asp Val Asn Ser Trp Cys Arg Arg Ala Arg Ala Lys
 210 215 220
 Ala Ala Ser Ala Gly Lys Lys Ala Ser Ser Ala Ala Pro His Thr
 225 230 235 240
 Val Ser Tyr Pro Asp Asn Leu Thr Tyr Arg Asp Leu Tyr Tyr Phe Leu
 245 250 255
 Phe Ala Pro Thr Leu Cys Tyr Glu Leu Asn Phe Pro Arg Ser Pro Arg
 260 265 270
 Ile Arg Lys Arg Phe Leu Leu Arg Arg Ile Leu Glu Met Leu Phe Phe
 275 280 285
 Thr Gln Leu Gln Val Gly Leu Ile Gln Gln Trp Met Val Pro Thr Ile
 290 295 300
 Gln Asn Ser Met Lys Pro Phe Lys Asp Met Asp Tyr Ser Arg Ile Ile
 305 310 315 320
 Glu Arg Leu Leu Lys Leu Ala Val Pro Asn His Leu Ile Trp Leu Ile
 325 330 335
 Phe Phe Tyr Trp Leu Phe His Ser Cys Leu Asn Ala Val Ala Glu Leu
 340 345 350
 Met Gln Phe Gly Asp Arg Glu Phe Tyr Arg Asp Trp Trp Asn Ser Glu
 355 360 365
 Ser Val Thr Tyr Phe Trp Gln Asn Trp Asn Ile Pro Val His Lys Trp
 370 375 380
 Cys Ile Arg His Phe Tyr Lys Pro Met Leu Arg Arg Gly Ser Ser Lys
 385 390 395 400
 Trp Met Ala Arg Thr Gly Val Phe Leu Ala Ser Ala Phe Phe His Glu
 405 410 415

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Tyr Leu Val Ser Val Pro Leu Arg Met Phe Arg Leu Trp Ala Phe Thr
 420 425 430

Gly Met Met Ala Gln Ile Pro Leu Ala Trp Phe Val Gly Arg Phe Phe
 435 440 445

Gln Gly Asn Tyr Gly Asn Ala Ala Val Trp Leu Ser Leu Ile Ile Gly
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Gln Pro Ile Ala Val Leu Met Tyr Val His Asp Tyr Tyr Val Leu Asn
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Tyr Glu Ala Pro Ala Ala Glu Ala
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 <212> DNA
 <213> Arabidopsis thaliana

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 ttcaaagcaa agggggnttn cctggggnta aagntccang ggcccttggg gccanccaa 540
 aannttcccc cgggaaaggg ttgcccaccg ggggngaaa aanncccggg ggcaccncgg 600
 aattttggga acccgggggg ggccttttt 629

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 <213> Arabidopsis thaliana

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<210> 8
 <211> 341
 <212> PRT
 <213> Brassica napus

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Glu Lys Leu Val Leu Gln Lys Cys Ile Ser Glu Pro Val Val Ile Phe
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 Leu His Val Ile Ile Thr Met Thr Glu Val Leu Tyr Pro Val Tyr Val
 35 40 45
 Thr Leu Arg Cys Asp Ser Ala Phe Leu Ser Gly Asp Thr Leu Met Leu
 50 55 60
 Leu Thr Cys Ile Val Trp Leu Lys Leu Val Ser Tyr Ala His Thr Asn
 65 70 75 80
 Tyr Asp Ile Arg Thr Leu Ala Asn Ser Ser Asp Lys Ala Asn Pro Glu
 85 90 95
 Val Ser Tyr Tyr Val Ser Leu Lys Ser Leu Ala Tyr Phe Met Leu Ala
 100 105 110
 Pro Thr Leu Cys Tyr Gln Pro Ser Tyr Pro Arg Ser Pro Cys Ile Arg
 115 120 125
 Lys Gly Trp Val Ala Arg Gln Phe Ala Lys Leu Val Ile Phe Thr Gly
 130 135 140
 Leu Met Gly Phe Ile Ile Glu Gln Tyr Ile Asn Pro Ile Val Arg Asn
 145 150 155 160
 Ser Lys His Pro Leu Lys Gly Asp Leu Leu Tyr Ala Ile Glu Arg Val
 165 170 175
 Leu Lys Leu Ser Val Pro Asn Leu Tyr Val Trp Leu Cys Met Phe Tyr
 180 185 190
 Cys Phe Phe His Leu Trp Leu Asn Ile Leu Ala Glu Leu Leu Cys Phe
 195 200 205
 Gly Asp Arg Glu Phe Tyr Lys Asp Trp Trp Asn Ala Lys Ser Val Gly
 210 215 220
 Asp Tyr Trp Arg Met Trp Asn Met Pro Val His Lys Trp Met Val Arg
 225 230 235 240
 His Val Tyr Phe Pro Cys Leu Arg Ile Lys Ile Pro Lys Val Pro Ala
 245 250 255
 Ile Ile Ile Ala Phe Leu Val Ser Ala Val Phe His Glu Leu Cys Ile
 260 265 270
 Ala Val Pro Cys Arg Leu Phe Asn Leu Trp Ala Phe Met Gly Ile Met
 275 280 285
 Phe Gln Val Pro Leu Val Phe Ile Thr Asn Phe Leu Gln Glu Arg Phe
 290 295 300
 Gly Ser Met Val Gly Asn Met Ile Phe Gly Ser Ala Ser Cys Ile Phe
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Lys Gly Ser Met Ser
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<213> Brassica napus
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Ser Ser Asn Gly Leu Leu Ser Asp Thr Ser Pro Ser Asp Asp Val Gly
35 40 45

Ala Ala Ala Ala Glu Arg Asp Arg Val Asp Ser Ala Ala Glu Glu Glu
50 55 60

Ala Gln Gly Thr Ala Asn Leu Ala Gly Gly Asp Ala Glu Thr Arg Glu
65 70 75 80

Ser Ala Gly Gly Asp Val Arg Phe Thr Tyr Arg Pro Ser Val Pro Ala
85 90 95

His Arg Arg Thr Arg Glu Ser Pro Leu Ser Ser Asp Ala Ile Phe Lys
100 105 110

Gln Ser His Ala Gly Leu Phe Asn Leu Cys Val Val Val Leu Val Ala
115 120 125

Val Asn Ser Arg Leu Ile Ile Glu Asn Leu Met Lys Tyr Gly Trp Leu
130 135 140

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Ile Arg Thr Asp Phe Trp Phe Ser Ser Thr Ser Leu Arg Asp Trp Pro  
145                      150                      155                      160
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Leu Phe Met Cys Cys Leu Ser Leu Ser Val Phe Pro Leu Ala Ala Phe
165 170 175

Thr Val Glu Lys Met Val Leu Gln Lys Phe Ile Ser Glu Pro Val Ala
180 185 190

Ile Ile Leu His Val Ile Ile Thr Met Thr Glu Val Leu Tyr Pro Val
195 200 205

Tyr Val Thr Leu Arg Cys Asp Ser Ala Phe Leu Ser Gly Val Thr Leu
210 215 220

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Met Leu Leu Thr Cys Ile Val Trp Leu Lys Leu Val Ser Tyr Ala His
 225 230 235 240

Thr Ser Tyr Asp Ile Arg Thr Leu Ala Asn Ser Ala Asp Lys Val Asp
 245 250 255

Pro Glu Ile Ser Tyr Tyr Val Ser Leu Lys Ser Leu Ala Tyr Phe Met
 260 265 270

Val Ala Pro Thr Leu Cys Tyr Gln Pro Ser Tyr Pro Arg Ser Pro Cys
 275 280 285

Ile Arg Lys Gly Trp Val Ala Arg Gln Leu Ala Lys Leu Val Ile Phe
 290 295 300

Thr Gly Leu Met Gly Phe Ile Ile Glu Gln Tyr Ile Asn Pro Ile Val
 305 310 315 320

Arg Asn Ser Lys His Pro Leu Lys Gly Asp Leu Leu Tyr Ala Ile Glu
 325 330 335

Arg Val Leu Lys Leu Ser Val Pro Asn Leu Tyr Val Trp Leu Cys Met
 340 345 350

Phe Tyr Cys Phe Phe His Leu Trp Leu Asn Ile Leu Ala Glu Leu Leu
 355 360 365

Cys Phe Gly Asp Arg Glu Phe Tyr Lys Asp Trp Trp Asn Ala Lys Ser
 370 375 380

Val Gly Asp Tyr Trp Arg Met Trp Asn Met Pro Val His Lys Trp Met
 385 390 395 400

Val Arg His Val Tyr Phe Pro Cys Leu Arg Ile Lys Ile Pro Lys Val
 405 410 415

Pro Ala Ile Ile Ile Ala Phe Leu Val Ser Ala Val Phe His Glu Leu
 420 425 430

Cys Ile Ala Val Pro Cys Arg Leu Phe Asn Leu Trp Ala Phe Met Gly
 435 440 445

Ile Met Phe Gln Val Pro Leu Val Phe Ile Thr Asn Phe Leu Gln Glu
 450 455 460

Arg Phe Gly Ser Met Val Gly Asn Met Ile Phe Gly Ser Ala Ser Cys
 465 470 475 480

Ile Phe Gly Gln Pro Met Cys Gly Leu Leu Tyr Tyr His Asp Leu Met
 485 490 495

Asn Arg Lys Gly Ser Met Ser
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<210> 11
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<212> PRT
<213> Arabidopsis thaliana

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24

<210> 13
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<212> DNA
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<400> 13
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<223> Description of Artificial Sequence: Primer DGAT1

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<223> Description of Artificial Sequence: Primer DGAT2

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<210> 16
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<223> Description of Artificial Sequence: Primer DGAT3

<400> 16
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<210> 17
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15/20

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<210> 18

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<223> Description of Artificial Sequence: Primer A

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<210> 19

<211> 24

<212> DNA

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<223> Description of Artificial Sequence: Primer B

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<210> 20

<211> 21

<212> DNA

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<223> Description of Artificial Sequence: Primer C

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<210> 21

<211> 33

<212> DNA

<213> Artificial Sequence

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<210> 22

<211> 33

<212> DNA

<213> Artificial Sequence

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<220>

<223> Description of Artificial Sequence: Primer Gen 2

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<210> 23

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<212> DNA

<213> Arabidopsis thaliana

<400> 23

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<212> DNA

<213> Arabidopsis thaliana

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<210> 25

<211> 547

<212> PRT

<213> Arabidopsis thaliana

<400> 25

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          20             25             30

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Ser Asp Ser Ser Asn Gly Leu Leu Leu Ser Gly Ser Asp Asn Asn Ser
          35             40             45

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Pro Ser Asp Asp Val Gly Ala Pro Ala Asp Val Arg Asp Arg Ile Asp
          50             55             60

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Ser Val Val Asn Asp Asp Ala Gln Gly Thr Ala Asn Leu Ala Gly Asp
          65             70             75             80

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Asn Asn Gly Gly Gly Asp Asn Asn Gly Gly Gly Arg Gly Gly Gly Glu

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85

90

95

Gly	Arg	Gly	Asn	Ala	Asp	Ala	Thr	Phe	Thr	Tyr	Arg	Pro	Ser	Val	Pro	100	105	110
Ala	His	Arg	Arg	Ala	Arg	Glu	Ser	Pro	Leu	Ser	Ser	Asp	Ala	Ile	Phe	115	120	125
Lys	Gln	Ser	His	Ala	Gly	Leu	Phe	Asn	Leu	Cys	Val	Val	Val	Leu	Ile	130	135	140
Ala	Val	Asn	Ser	Arg	Leu	Ile	Ile	Glu	Asn	Leu	Met	Lys	Ser	His	Ala	145	150	155
Gly	Leu	Phe	Asn	Leu	Cys	Val	Val	Val	Leu	Ile	Ala	Val	Asn	Ser	Arg	165	170	175
Leu	Ile	Ile	Glu	Asn	Leu	Met	Lys	Tyr	Gly	Trp	Leu	Ile	Arg	Thr	Asp	180	185	190
Phe	Trp	Phe	Ser	Ser	Arg	Ser	Leu	Arg	Asp	Trp	Pro	Leu	Phe	Met	Cys	195	200	205
Cys	Ile	Ser	Leu	Ser	Ile	Phe	Pro	Leu	Ala	Ala	Phe	Thr	Val	Glu	Lys	210	215	220
Leu	Val	Leu	Gln	Lys	Tyr	Ile	Ser	Glu	Pro	Val	Val	Ile	Phe	Leu	His	225	230	235
Ile	Ile	Ile	Thr	Met	Thr	Glu	Val	Leu	Tyr	Pro	Val	Tyr	Val	Thr	Leu	245	250	255
Arg	Cys	Asp	Ser	Ala	Phe	Leu	Ser	Gly	Val	Thr	Leu	Met	Leu	Leu	Thr	260	265	270
Cys	Ile	Val	Trp	Leu	Lys	Leu	Val	Ser	Tyr	Ala	His	Thr	Ser	Tyr	Asp	275	280	285
Ile	Arg	Ser	Leu	Ala	Asn	Ala	Ala	Asp	Lys	Ala	Asn	Pro	Glu	Val	Ser	290	295	300
Tyr	Tyr	Val	Ser	Leu	Lys	Ser	Leu	Ala	Tyr	Phe	Met	Val	Ala	Pro	Thr	305	310	315
Leu	Cys	Tyr	Gln	Pro	Ser	Tyr	Pro	Arg	Ser	Ala	Cys	Ile	Arg	Lys	Gly	325	330	335
Trp	Val	Ala	Arg	Gln	Phe	Ala	Lys	Leu	Val	Ile	Phe	Thr	Gly	Phe	Met	340	345	350
Gly	Phe	Ile	Ile	Glu	Gln	Tyr	Ile	Asn	Pro	Ile	Val	Arg	Asn	Ser	Lys	355	360	365
His	Pro	Leu	Lys	Gly	Asp	Leu	Leu	Tyr	Ala	Ile	Glu	Arg	Val	Leu	Lys	370	375	380

20/20

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 385 390 395 400
 Phe His Leu Trp Leu Asn Ile Leu Ala Glu Leu Leu Cys Phe Gly Asp
 405 410 415
 Arg Glu Phe Tyr Lys Asp Trp Trp Asn Ala Lys Ser Val Gly Asp Tyr
 420 425 430
 Trp Arg Met Trp Asn Met Pro Val His Lys Trp Met Val Arg His Ile
 435 440 445
 Tyr Phe Pro Cys Leu Arg Ser Lys Ile Pro Lys Thr Leu Ala Ile Ile
 450 455 460
 Ile Ala Phe Leu Val Ser Ala Val Phe His Glu Leu Cys Ile Ala Val
 465 470 475 480
 Pro Cys Arg Leu Phe Lys Leu Trp Ala Phe Leu Gly Ile Met Phe Gln
 485 490 495
 Val Pro Leu Val Phe Ile Thr Asn Tyr Leu Gln Glu Arg Phe Gly Ser
 500 505 510
 Thr Val Gly Asn Met Ile Phe Trp Phe Ile Phe Cys Ile Phe Gly Gln
 515 520 525
 Pro Met Cys Val Leu Leu Tyr Tyr His Asp Leu Met Asn Arg Lys Gly
 530 535 540
 Ser Met Ser
 545

Original (for SUBMISSION) - printed on 16.12.1999 03:08:17 PM

0-1	Form - PCT/RO/134 (EASY) Indications Relating to Deposited Microorganism(s) or Other Biological Material (PCT Rule 13bis)	
0-1-1	Prepared using	PCT-EASY Version 2.90 (updated 15.10.1999)
0-2	International Application No.	
0-3	Applicant's or agent's file reference	43922-PT
1	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
1-1	page	32
1-2	line	19
1-3	Identification of Deposit	
1-3-1	Name of depositary institution	American Type Culture Collection
1-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
1-3-3	Date of deposit	29 November 1999 (29.11.1999)
1-3-4	Accession Number	ATCC PTA-988
1-4	Additional Indications	NONE
1-5	Designated States for Which Indications are Made	all designated States
1-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
2	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
2-1	page	32
2-2	line	20
2-3	Identification of Deposit	
2-3-1	Name of depositary institution	American Type Culture Collection
2-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
2-3-3	Date of deposit	29 November 1999 (29.11.1999)
2-3-4	Accession Number	ATCC PTA-989
2-4	Additional Indications	NONE
2-5	Designated States for Which Indications are Made	all designated States
2-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
3	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
3-1	page	32
3-2	line	21

Original (for **SUBMISSION**) - printed on 16.12.1999 03:08:17 PM

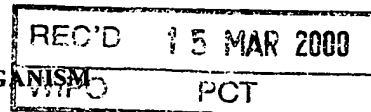
3-3	Identification of Deposit	
3-3-1	Name of depositary institution	American Type Culture Collection
3-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
3-3-3	Date of deposit	03 December 1999 (03.12.1999)
3-3-4	Accession Number	ATCC
3-4	Additional Indications	NONE
3-5	Designated States for Which Indications are Made	all designated States
3-6	Separate Furnishing of Indications	Accession number of Deposit dated Dec 3, 1999
	These indications will be submitted to the International Bureau later	

FOR RECEIVING OFFICE USE ONLY

0-4	This form was received with the international application: (yes or no)	yes
0-4-1	Authorized officer	Sophie hadreau

FOR INTERNATIONAL BUREAU USE ONLY

0-5	This form was received by the international Bureau on:	
0-5-1	Authorized officer	

INDICATIONS RELATING TO DEPOSITED MICROORGANISM
OR OTHER BIOLOGICAL MATERIAL

(PCT Rule 13bis)

A. The indications made below relate to the deposited microorganism or other biological material referred to in the description on page <u>32</u> , line <u>21</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution AMERICAN TYPE CULTURE COLLECTION	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209, U.S.A.	
Date of deposit December 3, 1999	Accession Number PTA-1013
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g. "Accession Number of Deposit") 	

For receiving Office use only
<input type="checkbox"/> This sheet was received with the international application
Authorized officer

For International Bureau use only
<input type="checkbox"/> This sheet was received by the International Bureau on:
Authorized officer

INTERNATIONAL SEARCH REPORT

International Application No

PCT/CA 99/01202

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/54 C12N15/82 A01H5/00 A01H5/10 A01H3/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N A01H

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	R61u012 Database Entry Ac005917 Accession number AC005917; 4 November 1998 LIN X. ET AL.: "Arabidopsis thaliana chromosome II section 113 of 255 of the complete sequence" XP002133608 nucleotides 21090-23400 -& LIN X. ET AL. : "Sequence and analysis of chromosome II of Arabidopsis thaliana" NATURE, vol. 402, 1999, pages 761-768, XP000877287 LONDON GB --- -/--	1-4,6-8, 10-13, 19-23

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents :

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

T later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

X document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

Y document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

G document member of the same patent family

Date of the actual completion of the international search

30 March 2000

Date of mailing of the international search report

14/04/2000

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
Fax: (+31-70) 340-3016

Authorized officer

Montero Lopez, B

INTERNATIONAL SEARCH REPORT

International Application No

PCT/CA 99/01202

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>CASES S ET AL: "Identification of a gene encoding an acyl CoA: diacylglycerol acyltransferase, a key enzyme in triacylglycerol synthesis"</p> <p>PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, US, NATIONAL ACADEMY OF SCIENCE. WASHINGTON, vol. 95, no. 22, 27 October 1998 (1998-10-27), pages 13018-13023, XP002122745</p> <p>ISSN: 0027-8424</p> <p>cited in the application</p> <p>the whole document</p>	1,2,22
X	<p>---</p> <p>VESNA KATAVIC ET AL.: "Alteration of seed fatty acid composition by an ethyl methanesulfonate-induced mutation in Arabidopsis thaliana affecting diacylglycerol acyltransferase activity"</p> <p>PLANT PHYSIOLOGY, vol. 108, 1995, pages 399-409, XP002915657</p> <p>cited in the application</p> <p>page 399, right-hand column, last paragraph -page 400, left-hand column, paragraph 1</p> <p>page 402, left-hand column, paragraph 2 -right-hand column, paragraph 1</p> <p>page 403, right-hand column, last paragraph -left-hand column, paragraph 1</p> <p>page 405, right-hand column, last paragraph -page 408, left-hand column, paragraph 1</p>	10-18
E	<p>---</p> <p>WO 99 67403 A (THE REGENTS OF THE UNIVERSITY OF CALIFORNIA)</p> <p>29 December 1999 (1999-12-29)</p> <p>page 3, line 27 -page 6, line 5</p> <p>page 10, line 2 - line 25</p> <p>page 14, line 16 - line 21</p> <p>page 15, line 24 -page 16, line 28</p> <p>page 33, line 4 - line 32</p> <p>page 39, line 28 -page 40, line 11</p>	1-4,6, 10,12, 19-23
E	<p>---</p> <p>WO 00 01713 A (CALGENE LLC)</p> <p>13 January 2000 (2000-01-13)</p> <p>page 4, line 10 - line 17</p> <p>page 4, line 20 -page 5, line 2</p> <p>page 11, line 27 -page 24, line 21;</p> <p>examples 11-14,16</p> <p>---</p> <p style="text-align: center;">-/--</p>	1-4,6, 10,12, 19,22,23

INTERNATIONAL SEARCH REPORT

International Application No

PCT/CA 99/01202

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	<p>Empln Database Entry Ath238008 Accession number AJ238008; 18 June 1999 ZOU J. ET AL.: "The Arabidopsis thaliana TAG1 gene encodes for a diacylglycerol acyltransferase" XP002133609 cited in the application the whole document</p> <p style="text-align: center;">---</p>	1,2,22
P,X	<p>ZOU, JITAO ET AL: "The Arabidopsis thaliana TAG1 mutant has a mutation in a diacylglycerol acyltransferase gene" PLANT J. (1999), 19(6), 645-653 , XP002133607 the whole document</p> <p style="text-align: center;">---</p>	1,2,22
P,X	<p>EMBL Database Entry AF155224 Accession number AF155224; 30 June 1999 NYKIFORUK C.L. ET AL.: "Brassica napus putative diacylglycerol cyltransferase (DGAT2) mRNA" XP002133639 cited in the application the whole document & NYKIFORUK C.L. ET AL.: "Isolation and sequence analysis of a novel cDNA encoding a putative diacylglycerol acyltransferase from a microspore-derived cell suspension culture of Brassica napus L. cv Jet Neuf (Accession No. AF155224) (PGR99-123)." PLANT PHYSIOLOGY, vol. 120, no. 4, 1999, pages 1207-1207, LONDON GB</p> <p style="text-align: center;">---</p>	1,2,22
P,X	<p>EMBL Database Entry AF164434 Accession number AF164434; 26 July 1999 NYKIFORUK C.L. ET AL.: "Brassica napus putative diacylglycerol acyltransferase (DGAT1) mRNA" XP002133640 cited in the application the whole document & NYKIFORUK C.L. ET AL.: "Isolation and characterization of a cDNA encoding a second putative diacylglycerol acyltransferase from a microspore-derived cell suspension culture of Brassica napus L. cv Jet Neuf (Accession No. AF164434) (PGR99-158)" PLANT PHYSIOLOGY, vol. 121, no. 3, 1999, pages 1053-1053,</p> <p style="text-align: center;">---</p> <p style="text-align: center;">-/--</p>	1,2,22

INTERNATIONAL SEARCH REPORT

International Application No

PCT/CA 99/01202

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	<p>HOBBS D H ET AL: "Cloning of a cDNA encoding diacylglycerol acyltransferase from Arabidopsis thaliana and its functional expression" FEBS LETTERS,NL,ELSEVIER SCIENCE PUBLISHERS, AMSTERDAM, vol. 452, no. 3, 11 June 1999 (1999-06-11), pages 145-149, XP002122747 ISSN: 0014-5793 the whole document</p>	1,2,22
P,X	<p>WO 99 63096 A (CALGENE LLC) 9 December 1999 (1999-12-09)</p> <p>page 3, line 24 -page 4, line 17 page 6, line 13 -page 8, line 16 page 12, line 30 -page 20, line 10; examples 1-4,7,8 sequence listing SEQ ID NO:1</p>	1-4,6, 10-13, 19,22,23

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/CA 99/01202

Patent document cited in search report		Publication date	Patent family member(s)	Publication date
WO 9967403	A	29-12-1999	WO 9967268 A	29-12-1999
WO 0001713	A	13-01-2000	NONE	
WO 9963096	A	09-12-1999	NONE	

PATENT COOPERATION TREATY

PCT

NOTIFICATION OF ELECTION

(PCT Rule 61.2)

From the INTERNATIONAL BUREAU

To:

Assistant Commissioner for Patents
United States Patent and Trademark
Office
Box PCT
Washington, D.C.20231
ETATS-UNIS D'AMERIQUE

in its capacity as elected Office

Date of mailing (day/month/year) 21 August 2000 (21.08.00)	
International application No. PCT/CA99/01202	Applicant's or agent's file reference 43922-PT
International filing date (day/month/year) 16 December 1999 (16.12.99)	Priority date (day/month/year) 17 December 1998 (17.12.98)
Applicant ZOU, Jitao et al	

1. The designated Office is hereby notified of its election made:

☒ in the demand filed with the International Preliminary Examining Authority on:
14 July 2000 (14.07.00)

☐ in a notice effecting later election filed with the International Bureau on:

2. The election ☒ was
☐ was not

made before the expiration of 19 months from the priority date or, where Rule 32 applies, within the time limit under Rule 32.2(b).

The International Bureau of WIPO 34, chemin des Colombettes 1211 Geneva 20, Switzerland Facsimile No.: (41-22) 740.14.35	Authorized officer Nestor Santesso Telephone No.: (41-22) 338.83.38
---	---

NOTES TO FORM PCT/ISA/220

These Notes are intended to give the basic instructions concerning the filing of amendments under article 19. The Notes are based on the requirements of the Patent Cooperation Treaty, the Regulations and the Administrative Instructions under that Treaty. In case of discrepancy between these Notes and those requirements, the latter are applicable. For more detailed information, see also the PCT Applicant's Guide, a publication of WIPO.

In these Notes, "Article", "Rule", and "Section" refer to the provisions of the PCT, the PCT Regulations and the PCT Administrative Instructions respectively.

INSTRUCTIONS CONCERNING AMENDMENTS UNDER ARTICLE 19

The applicant has, after having received the international search report, one opportunity to amend the claims of the international application. It should however be emphasized that, since all parts of the international application (claims, description and drawings) may be amended during the international preliminary examination procedure, there is usually no need to file amendments of the claims under Article 19 except where, e.g. the applicant wants the latter to be published for the purposes of provisional protection or has another reason for amending the claims before international publication. Furthermore, it should be emphasized that provisional protection is available in some States only.

What parts of the international application may be amended?

Under Article 19, only the claims may be amended.

During the international phase, the claims may also be amended (or further amended) under Article 34 before the International Preliminary Examining Authority. The description and drawings may only be amended under Article 34 before the International Examining Authority.

Upon entry into the national phase, all parts of the international application may be amended under Article 28 or, where applicable, Article 41.

When?

Within 2 months from the date of transmittal of the international search report or 16 months from the priority date, whichever time limit expires later. It should be noted, however, that the amendments will be considered as having been received on time if they are received by the International Bureau after the expiration of the applicable time limit but before the completion of the technical preparations for international publication (Rule 46.1).

Where not to file the amendments?

The amendments may only be filed with the International Bureau and not with the receiving Office or the International Searching Authority (Rule 46.2).

Where a demand for international preliminary examination has been/is filed, see below.

How?

Either by cancelling one or more entire claims, by adding one or more new claims or by amending the text of one or more of the claims as filed.

A replacement sheet must be submitted for each sheet of the claims which, on account of an amendment or amendments, differs from the sheet originally filed.

All the claims appearing on a replacement sheet must be numbered in Arabic numerals. Where a claim is cancelled, no renumbering of the other claims is required. In all cases where claims are renumbered, they must be renumbered consecutively (Administrative Instructions, Section 205(b)).

The amendments must be made in the language in which the international application is to be published.

What documents must/may accompany the amendments?

Letter (Section 205(b)):

The amendments must be submitted with a letter.

The letter will not be published with the international application and the amended claims. It should not be confused with the "Statement under Article 19(1)" (see below, under "Statement under Article 19(1)").

The letter must be in English or French, at the choice of the applicant. However, if the language of the international application is English, the letter must be in English; if the language of the international application is French, the letter must be in French.

NOTES TO FORM PCT/ISA/220 (continued)

The letter must indicate the differences between the claims as filed and the claims as amended. It must, in particular, indicate, in connection with each claim appearing in the international application (it being understood that identical indications concerning several claims may be grouped), whether

- (i) the claim is unchanged;
- (ii) the claim is cancelled;
- (iii) the claim is new;
- (iv) the claim replaces one or more claims as filed;
- (v) the claim is the result of the division of a claim as filed.

The following examples illustrate the manner in which amendments must be explained in the accompanying letter:

1. [Where originally there were 48 claims and after amendment of some claims there are 51]:
"Claims 1 to 29, 31, 32, 34, 35, 37 to 48 replaced by amended claims bearing the same numbers; claims 30, 33 and 36 unchanged; new claims 49 to 51 added."
2. [Where originally there were 15 claims and after amendment of all claims there are 11]:
"Claims 1 to 15 replaced by amended claims 1 to 11."
3. [Where originally there were 14 claims and the amendments consist in cancelling some claims and in adding new claims]:
"Claims 1 to 6 and 14 unchanged; claims 7 to 13 cancelled; new claims 15, 16 and 17 added." or
"Claims 7 to 13 cancelled; new claims 15, 16 and 17 added; all other claims unchanged."
4. [Where various kinds of amendments are made]:
"Claims 1-10 unchanged; claims 11 to 13, 18 and 19 cancelled; claims 14, 15 and 16 replaced by amended claim 14; claim 17 subdivided into amended claims 15, 16 and 17; new claims 20 and 21 added."

"Statement under article 19(1)" (Rule 46.4)

The amendments may be accompanied by a statement explaining the amendments and indicating any impact that such amendments might have on the description and the drawings (which cannot be amended under Article 19(1)).

The statement will be published with the international application and the amended claims.

It must be in the language in which the international application is to be published.

It must be brief, not exceeding 500 words if in English or if translated into English.

It should not be confused with and does not replace the letter indicating the differences between the claims as filed and as amended. It must be filed on a separate sheet and must be identified as such by a heading, preferably by using the words "Statement under Article 19(1)."

It may not contain any disparaging comments on the international search report or the relevance of citations contained in that report. Reference to citations, relevant to a given claim, contained in the international search report may be made only in connection with an amendment of that claim.

Consequence if a demand for international preliminary examination has already been filed

If, at the time of filing any amendments under Article 19, a demand for international preliminary examination has already been submitted, the applicant must preferably, at the same time of filing the amendments with the International Bureau, also file a copy of such amendments with the International Preliminary Examining Authority (see Rule 62.2(a), first sentence).

Consequence with regard to translation of the international application for entry into the national phase

The applicant's attention is drawn to the fact that, where upon entry into the national phase, a translation of the claims as amended under Article 19 may have to be furnished to the designated/elected Offices, instead of, or in addition to, the translation of the claims as filed.

For further details on the requirements of each designated/elected Office, see Volume II of the PCT Applicant's Guide.